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A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA LIBRARY. APPLICATION TO THE DETECTION OF MYCOBACTERIA.

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I. Background of the invention

[001] The present invention pertains to a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given [mycobacterium] strain, said DNA library being cloned in a bacterial artificial chromosome (BAC). The invention concerns also polynucleotides identified by the above method, as well as detection methods for mycobacteria, particularly *Mycobacterium tuberculosis*, and kits using said polynucleotides as primers or probes. Finally, the invention deals with BAC-based mycobacterium DNA libraries used in the method according to the invention and particularly BAC-based *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG DNA libraries.

[002] Radical measures are required to prevent the grim predictions of the World Health Organisation for the evolution of the global tuberculosis epidemic in the next century becoming a tragic reality. The powerful combination of genomics and bioinformatics is providing a wealth of information about the etiologic agent, *Mycobacterium tuberculosis*, that will facilitate the conception and development of new therapies. The start point for genome sequencing was the integrated map of the 4.4 Mb circular chromosome of the widely-used, virulent reference strain, *M. tuberculosis* H37Rv and appropriate cosmids were subjected to systematic shotgun sequence analysis at the Sanger Centre.

[003] Cosmid clones (Balasubramanian et al., 1996; Pavelka et al., 1996) have played a crucial role in the *M. tuberculosis* H37Rv genome sequencing project. However, problems such as under-representation of certain regions of the chromosome, unstable inserts and the relatively small insert size complicated the production of a comprehensive set of canonical cosmids representing the entire genome.

II. Summary of the invention

[004] In order to avoid the numerous technical constraints encountered in the state of the art, as described hereabove, when using genomic mycobacterial DNA libraries constructed in cosmid clones, the inventors have attempted to realize genomic mycobacterial DNA libraries in an alternative type of vectors, namely Bacterial Artificial Chromosome (BAC) vectors.

[005] The success of this approach depended on whether the resulting BAC clones could maintain large mycobacterial DNA inserts. There are various reports describing the successful construction of a BAC library for eucaryotic organisms (Cai et al., 1995; Kim et al., 1996; Misumi et al., 1997; Woo et al., 1994; Zimmer et al., 1997) where inserts up to 725 kb (Zimmer et al., 1997) were cloned and stably maintained in the *E. coli* host strain.

[006] Here, it is shown that, surprisingly, the BAC system can also be used for mycobacterial DNA, as 70% of the clones contained inserts in the size of 25 to 104 kb.

[007] This is the first time that bacterial, and specifically mycobacterial, DNA is cloned in such BAC vectors.

[008] In an attempt to obtain complete coverage of the genome with a minimal overlapping set of clones, a Bacterial Artificial Chromosome (BAC) library of *M. tuberculosis* was constructed, using the vector pBeloBAC11 (Kim et al., 1996) which combines a simple phenotypic screen for recombinant clones with the stable propagation of large inserts (Shizuya et al., 1992). The BAC cloning system is based on the *E. coli* F-factor, whose replication is strictly controlled and thus ensures stable maintenance of large constructs (Willets et al., 1987).

[009] BACs have been widely used for cloning of DNA from various eucaryotic species (Cai et al., 1995; Kim et al., 1996; Misumi et al., 1997; Woo et al., 1994; Zimmer et al., 1997). In contrast, to our knowledge this report describes the first attempt to use the BAC system for cloning bacterial DNA.

[010] A central advantage of the BAC cloning system over cosmid vectors used in prior art is that the F-plasmid is present in only one or a maximum of two copies per cell, reducing the potential for recombination between DNA fragments and, more importantly, avoiding the lethal overexpression of cloned bacterial genes. However, the presence of the BAC as just a single copy means that plasmid DNA has to be extracted from a large volume of culture to obtain

sufficient DNA for sequencing and it is described here in the examples a simplified protocol to achieve this.

5 [010] Further, the stability and fidelity of maintenance of the clones in the BAC library represent ideal characteristics for the identification of genomic differences possibly responsible for phenotypic variations in different mycobacterial species.

[011] As it will be shown herein, BACs can be allied with conventional hybridization techniques for refined analyses of genomes and transcriptional activity from different mycobacterial species.

10 [012] Having established a reliable procedure to screen for genomic polymorphisms, it is now possible to conduct these comparisons on a more systematic basis than in prior art using representative BACs throughout the chromosome and genomic DNA from a variety of mycobacterial species.

15 [013] As another approach to display genomic polymorphisms, the inventors have also started to use selected H37Rv BACs for "molecular combing" experiments in combination with fluorescent *in situ* hybridization (Bensimon et al., 1994; Michalet et al., 1997). With such techniques the one skilled in the art is enabled to explore the genome of mycobacteria in general and of *M. tuberculosis* in particular for further polymorphic regions.

20 [014] The availability of BAC-based genomic mycobacterial DNA libraries constructed by the inventors have allowed them to design methods and means both useful to identify genomic regions of interest of pathogenic mycobacteria, such as *Mycobacterium tuberculosis*, that have no counterpart in the corresponding non-pathogenic strains, such as *Mycobacterium bovis* BCG, and useful to detect the presence of polynucleotides belonging to a specific mycobacterium strain in a biological sample.

25 [015] By a biological sample according to the present invention, it is notably intended a biological fluid, such as plasma, blood, urine or saliva, or a tissue, such as a biopsy.

30 [016] Thus, a first object of the invention consists of a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, 35 said DNA library being cloned in a bacterial artificial chromosome (BAC).

[017] The invention is also directed to a polynucleotide of interest that has been isolated according to the above method and in [particular] a polynucleotide containing one or several Open Reading Frames (ORFs), for example ORFs encoding either a polypeptide involved in the pathogenicity of a mycobacterium strain or ORFs encoding Polymorphic Glycine Rich Sequences (PGRS).

5 [018] Such polynucleotides of interest may serve as probes or primers in order to detect the presence of a specific myobacterium strain in a biological sample or to detect the expression of specific genes in a particular mycobacterial strain of interest.

10 [019] The BAC-based genomic mycobacterial DNA libraries generated by the present inventors are also part of the invention, as well as each of the recombinant BAC clones and the DNA insert contained in each of said recombinant BAC clones.

15 [020] The invention also pertains to methods and kits for detecting a specific mycobacterium in a biological sample using either at least one recombinant BAC clone or at least one polynucleotide according to the invention, as well as to methods and kits to detect the expression of one or several specific genes of a given mycobacterial strain present in a biological sample.

20 III. Brief description of the Figures.

[021] In order to better understand the present invention, reference will be made to the appended figures which depicted specific embodiments to which the present invention is in no case limited in scope with.

25 [022] Figures 1A and 1B : PCR-screening for unique BAC clones with specific primers for 2 selected genomic regions of the H37Rv chromosome, using 21 pools representing 2016 BACs (Figure 1A) and sets of 20 subpools from selected positive pools (Figure 1B).

[023] Figure 2 : Pulsed-field gel electrophoresis gel of *Dra*I- cleaved BAC clones used 30 for estimating the insert sizes of BACs.

[024] Figure 3 : Minimal overlapping BAC map of *M. tuberculosis* H37Rv superimposed on the integrated physical and genetic map established by Philipp et al. (18). Y- and I- numbers show pYUB328 (2) and pYUB412 (16) cosmids which were shotgun sequenced during the H37Rv genome sequencing project. Y- 35 cosmids marked with * were shown in the integrated physical and genetic map

(18). Rv numbers show the position of representative BAC clones relative to sequenced Y- and I- clones. Squared Rv numbers show BACs which were shotgun sequenced at the Sanger Centre.

[025] Figures 4A and 4B : Ethidium bromide stained gel (Figure 4A) and 5 corresponding Southern blot (Figure 4B) of *Eco*RI and *Pvu*II digested Rv58 DNA hybridized with ³²P labeled genomic DNA preparations from *M. tuberculosis* H37Rv, *M. bovis* ATCC 19210 and *M. bovis* BCG Pasteur.

[026] Figure 5 : Organisation of the ORFs in the 12.7 kb genomic region present in *M. tuberculosis* H37Rv but not present in *M. bovis* ATCC 19210 and *M. bovis* BCG 10 Pasteur. Arrows show the direction of transcription of the putative genes. Positions of *Eco*RI and *Pvu*II restriction sites are shown. Vertical dashes represent stop codons. The 11 ORFs correspond to the ORFs MTCY277.28 to MTCY277.38 / accession number Z79701 -EMBL Nucleotide Sequence Data Library. The junction sequences flanking the polymorphic region are shown.

[027] Figure 6 : Variation in the C-terminal part of a PE-PGRS open reading frame in *M. tuberculosis* strain H37Rv relative to *M. bovis* BCG strain Pasteur.

[028] The numbers on the right side of the Figure denote the position of the end nucleotides, taking as the reference the *M. tuberculosis* genome.

[029] Figure 7 : Polynucleotide sequence next to the HindIII cloning site in the BAC 20 vector pBeloBAC11 (Kim et al., 1996) used to clone the inserts of the BAC-based myobacterial genomic DNA library according to the invention.

[030] NotI : location of the NotI restriction sites.

[031] Primer T7-BAC1 : nucleotide region recognized by the T7-BAC1 primer shown in Table 1.

[032] T7 promoter : location of the T7 promoter region on the pBeloBac11 vector.

[033] Primer T7-Belo2 : nucleotide region recognized by the T7-Belo2 primer shown in Table 1.

[034] Hind III : the HindIII cloning site used to clone the genomic inserts in the pBeloBAC11 vector.

[035] SP6-Mid primer : nucleotide region recognized by the SP6 Mid primer shown in Table 1.

[036] SP6-BAC1 primer : nucleotide region recognized by the SP6 BAC1 primer shown in Table 1.

SP6 promoter : location of the SP6 promoter region [on the] pBeloBac11 vector.

IV. Detailed description of the preferred embodiments.

[D38] As already mentioned hereinbefore, the present invention is directed to a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC) type vector.

10 [D39] For this purpose, the inventors have constructed several BAC-based mycobacterial genomic DNA libraries that may be used in order to perform the above described method.

15 [D40] Because it is the first time that mycobacterial genomic DNA has been successfully cloned in BAC type vectors, and because these DNA libraries are then novel and nonobvious, an object of the present invention consists in a mycobacterial genomic DNA library cloned in such a BAC type vector.

20 [D41] As an illustrative example, a BAC-based DNA library of *Mycobacterium tuberculosis* has been realized. Forty-seven cosmids chosen from the integrated map of the 4.4 Mb circular chromosome (Philipp et al., 1996a) were shotgun-sequenced during the initial phase of the H37Rv genome sequence project. The sequences of these clones were used as landmarks in the construction of a minimally overlapping BAC map. Comparison of the sequence data from the termini of 420 BAC clones allowed us to establish a minimal overlapping BAC map and to fill in the existing gaps between the sequence of cosmids. As well as 25 using the BAC library for genomic mapping and sequencing, we also tested the system in comparative genomic experiments in order to uncover differences between two closely related mycobacterial species. As shown in a previous study (Philipp et al., 1996b), *M. tuberculosis*, *M. bovis* and *M. bovis* BCG, specifically BCG Pasteur strain, exhibit a high level of global genomic conservation, but 30 certain polymorphic regions were also detected. Therefore, it was of great interest to find a reliable, easy and rapid way to exactly localize polymorphic regions in mycobacterial genomes using selected BAC clones. This approach was validated by determining the exact size and location of the polymorphisms in the genomic region of *Dra*I fragment Z4 (Philipp et al., 1996b), taking advantage of the 35 availability of an appropriate BAC clone covering the polymorphic region and

the H37Rv genome sequence data. This region is located approximately 1.7 Mb from the origin of replication.

[D42] The Bacterial Artificial Chromosome (BAC) cloning system is capable of stably propagating large, complex DNA inserts in *Escherichia coli*. As part of the

5 *Mycobacterium tuberculosis* H37Rv genome sequencing project, a BAC library was constructed in the pBeloBAC11 vector and used for genome mapping, confirmation of sequence assembly, and sequencing. The library contains about 5000 BAC clones, with inserts ranging in size from 25 to 104 kb, representing theoretically a 70 fold coverage of the *M. tuberculosis* genome (4.4 Mb). A total

10 of 840 sequences from the T7 and SP6 termini of 420 BACs were determined and compared to those of a partial genomic database. These sequences showed excellent correlation between the estimated sizes and positions of the BAC clones and the sizes and positions of previously sequenced cosmids and the resulting contigs. Many BAC clones represent linking clones between sequenced cosmids,

15 allowing full coverage of the H37Rv chromosome, and they are now being shotgun-sequenced in the framework of the H37Rv sequencing project. Also, no chimeric, deleted or rearranged BAC clones were detected, which was of major importance for the correct mapping and assembly of the H37Rv sequence. The minimal overlapping set contains 68 unique BAC clones and spans the whole

20 H37Rv chromosome with the exception of a single gap of ~ 150 kb. As a post-genomic application, the canonical BAC set was used in a comparative study to reveal chromosomal polymorphisms between *M. tuberculosis*, *M. bovis* and *M. bovis* BCG Pasteur, and a novel 12.7 kb segment present in *M. tuberculosis* but absent from *M. bovis* and *M. bovis* BCG was characterized. This region contains

25 a set of genes whose products show low similarity to proteins involved in polysaccharide biosynthesis. The H37Rv BAC library therefore provides the one skilled in the art with a powerful tool both for the generation and confirmation of sequence data as well as for comparative genomics and a plurality of post-genomic applications.

30 [D43] The above described BAC-based *Mycobacterium tuberculosis* genomic DNA library is part of the present invention and has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on November 19, 1997 under the accession number I-1945.

[D44] Another BAC-based DNA library has been constructed with the genomic DNA of *Mycobacterium bovis* BCG, Pasteur strain, and said DNA library has

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been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on [XX XX] 1998 under the accession number I-[XXXX] 2049

[045] Thus, as a specific embodiment of the above described method for isolating a polynucleotide of interest said method makes use of at least one BAC-based DNA library that has been constructed from the genomic DNA of *Mycobacterium tuberculosis*, more specifically of the H37Rv strain and particularly of the DNA library deposited in the accession number I-1945.

[046] In another specific embodiment of the above described method for isolating a polynucleotide of interest said method makes use of at least one BAC-based DNA library has been constructed from the genomic DNA of *Mycobacterium bovis* BCG, more specifically of the Pasteur strain and particularly of the DNA library deposited in the accession number I-[XXXX] 2049

[047] In more details, the method according to the invention for isolating a polynucleotide of interest may comprise the following steps :

15 [048] a) isolating at least one polynucleotide contained in a clone of a BAC-based DNA library of mycobacterial origin;

[049] b) isolating :

[050] - at least one genomic or cDNA polynucleotide from a mycobacterium, said mycobacterium belonging to a strain different from the strain used to construct 20 the BAC-based DNA library of step a); or alternatively

[051] - at least one polynucleotide contained in a clone of a BAC-based DNA library prepared from the genome of a mycobacterium that is different from the mycobacterium used to construct the BAC-based DNA library of step a);

[052] c) hybridizing the at least one polynucleotide of step a) to the at least one 25 polynucleotide of step b);

[053] d) selecting the at least one polynucleotide of step a) that has not formed a hybrid complex with the at least one polynucleotide of step b);

[054] e) characterizing the selected polynucleotide.

[055] Following the above procedure, the at least one polynucleotide of step a) 30 may be prepared as follows :

[056] 1) digesting at least one recombinant BAC clone by an appropriate restriction endonuclease in order to isolate the polynucleotide insert of interest from the vector genetic material;

[057] 2) optionally amplifying the resulting polynucleotide insert;

3) optionally digesting the polynucleotide insert of step 1) or step 2) with at least one restriction endonuclease.

[059] The above method of the invention allows the one skilled in the art to perform comparative genomics between different strains or species of mycobacteria cells, for example between pathogenic strains or species and their non pathogenic strains or species counterparts, as it is the illustrative case for the genomic comparison between *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG that is described herein in the examples.

[060] Restriction digests of a given clone of a BAC library according to the invention may be blotted to membranes, and then probed with radiolabeled DNA from another strain or another species of mycobacteria, allowing the one skilled in the art to identify, characterize and isolate a polynucleotide of interest that may be involved in important metabolical and/or physiological pathways of the mycobacterium under testing, such as a polynucleotide functionally involved in the pathogenicity of said given mycobacteria for its host organism.

[061] More specifically, the inventors have shown in Example 6 that when restriction digests of a given clone of the BAC library identified by the CNCM accession number I-1945 are blotted to membranes and then probed with radiolabeled total genomic DNA from, for example, *Mycobacterium bovis* BCG Pasteur, it is observed that restriction fragments that fail to hybridize with the *M. bovis* BCG Pasteur DNA are absent from its genome, hence identifying polymorphic regions between *M. bovis* BCG Pasteur and *M. tuberculosis* H37Rv.

[062] Thus, a further object of the present invention consists in a polynucleotide of interest that has been isolated according to the method described herein before.

[063] In Example 6, a polynucleotide of approximately 12.7 kilobases has been isolated that is present in the genome of *M. tuberculosis* but is absent of the genome of *M. bovis* BCG. This polynucleotide of interest contains 11 ORFs that may be involved in polysaccharide biosynthesis. In particular, two of said ORFs are of particular interest, namely ORF6 (MTCY277.33; Rv1511) that encodes a protein that shares significant homology with bacterial GDP-D-mannose dehydratases, whereas the protein encoded by ORF7 (MTCY277.34; Rv1512) shares significant homology with a nucleotide sugar epimerase. As polysaccharide is a major constituent of the mycobacterial cell wall, these deleted genes may cause the cell wall of *M. bovis* BCG to differ from that of *M. tuberculosis*, a fact that may have important consequences for both the immune

response to *M. bovis* BCG and virulence. Detection of such a polysaccharide is of diagnostic interest and possibly useful in the design of tuberculosis vaccines.

[D64] Consequently, the polynucleotide of interest obtained following the method according to the invention may contain at least one ORF, said ORF 5 preferably encoding all or part of a polypeptide involved in an important metabolical and/or physiological pathway of the mycobacteria under testing, and more specifically all or part of a polypeptide that is involved in the pathogenicity of the mycobacteria under testing, such as for example *Mycobacterium tuberculosis*, and more generally mycobacteria belonging to the *Mycobacterium tuberculosis* complex. 10

[D65] The *Mycobacterium tuberculosis* complex has its usual meaning, i.e. the complex of mycobacteria causing tuberculosis which are *Mycobacterium tuberculosis*, *Mycobacterium bovis*, *Mycobacterium africanum*, *Mycobacterium microti* and the vaccine strain *Mycobacterium bovis* BCG.

[D66] An illustrative polynucleotide of interest according to the present invention comprises all or part of the polynucleotide of approximately 12.7 kilobases that is present in the genome of *M. tuberculosis* but is absent from the genome of *M. bovis* BCG disclosed hereinbefore. This polynucleotide is contained in clone Rv58 of the BAC DNA library I-1945.

[D67] Generally, the invention also pertains to a purified polynucleotide comprising the DNA insert contained in a recombinant BAC vector belonging to a BAC-based mycobacterial genomic DNA library, such as for example the I-1945 BAC DNA library.

[D68] Advantageously, such a polynucleotide has been identified according to 25 the method of the invention.

[D69] Such a polynucleotide of interest may be used as a probe or a primer useful for specifically detecting a given mycobacterium of interest, such as *Mycobacterium tuberculosis* or *Mycobacterium bovis* BCG.

[D70] More specifically, the invention then deals with a purified polynucleotide 30 useful as probe or a primer comprising all or part of the nucleotide sequence SEQ ID N°1.

[D71] The location, on the *Mycobacterium tuberculosis* chromosome, of the above polynucleotide of sequence SEQ ID N°1 has now been ascribed to begin, at its 5'end at nucleotide at position nt 1696015 and to end, at its 3'end, at 35 nucleotide at position nt 1708746.

[D72] For diagnostic purposes, this 12.7 kb deletion should allow a rapid PCR screening of tubercle isolates to identify whether they are bovine or human strains. The primers listed in Table 1 are flanking the deleted region and give a 722 bp amplicon in *M. bovis* or *M. bovis* BCG strains, but a fragment of 13,453 bp in *M. tuberculosis* that is practically impossible to amplify under the same PCR conditions. More importantly, assuming that some of the gene products from this region represent proteins with antigenic properties, it could be possible to develop a test that can reliably distinguish between the immune response induced by vaccination with *M. bovis* BCG vaccine strains and infection with *M. tuberculosis* or that the products (e.g. polysaccharides) are specific immunogens.

[D73] The invention also provides for a purified polynucleotide useful as a probe or as a primer, said polynucleotide being chosen in the following group of polynucleotides :

[D74] a) a polynucleotide comprising at least 8 consecutive nucleotides of the sequence 15 SEQ ID N°1;

[D75] b) a polynucleotide whose sequence is fully complementary to the sequence of the polynucleotide defined in a);

[D76] c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

20 [D77] For the purpose of defining a polynucleotide or oligonucleotide hybridizing under stringent hybridization conditions, such as above, it is intended a polynucleotide that hybridizes with a reference polynucleotide under the following hybridization conditions.

[D78] The hybridization step is realized at 65°C in the presence of 6 x SSC 25 buffer, 5 x Denhardt's solution, 0,5% SDS and 100µg/ml of salmon sperm DNA.

[D79] For technical information, 1 x SSC corresponds to 0.15 M NaCl and 0.05M sodium citrate; 1 x Denhardt's solution corresponds to 0.02% Ficoll, 0.02% polyvinylpyrrolidone and 0.02% bovine serum albumin.

[D80] The hybridization step is followed by four washing steps :

30 [D81] two washings during 5 min, preferably at 65°C in a 2 x SSC and 0.1%SDS buffer,

[D82] - one washing during 30 min, preferably at 65°C in a 2 x SSC and 0.1% SDS buffer,

[D83] - one washing during 10 min, preferably at 65°C in a 0.1 x SSC and 0.1%SDS 35 buffer.

[D84] A first illustrative useful polynucleotide that is included in the polynucleotide of sequence SEQ ID N°1 is the polynucleotide of sequence SEQ ID N°2 that corresponds to the Sp6 end-sequence of SEQ ID N°1.

[D85] A second illustrative useful polynucleotide that is included in the polynucleotide of sequence SEQ ID N°1 is the polynucleotide of sequence SEQ ID N°3 that corresponds to the T7 end-sequence of SEQ ID N°1, located on the opposite strand.

[D86] The polynucleotide of sequence SEQ ID N°1 contains 11 ORFs, the respective locations of which, taking into account the orientation of each ORF on the chromosome, on the sequence of the *Mycobacterium tunerculosis* chromosome, is given hereafter :

[D87] - The location of ORF1 is comprised between nucleotide at position nt 1695944 and nucleotide at position nt1696441.

[D88] - The location of ORF2 is comprised between nucleotide at position nt 1696728 and nucleotide at position nt1697420.

[D89] - The location of ORF3 is comprised between nucleotide at position nt 1698096 and nucleotide at position nt1699892. ORF3 probably encodes a protein having the characteristics of a membrane protein.

[D90] - The location of ORF4 is comprised between nucleotide at position nt 1700210 and nucleotide at position nt1701088.

[D91] - The location of ORF5 is comprised between nucleotide at position nt 1701293 and nucleotide at position nt1702588. ORF5 encodes a protein having the characteristics of a membrane protein.

[D92] - The location of ORF6 is comprised between nucleotide at position nt 1703072 and nucleotide at position nt1704091. ORF6 encodes a protein having the characteristics of a GDP-D-mannose dehydratase.

[D93] - The location of ORF7 is comprised between nucleotide at position nt 1704091 and nucleotide at position nt1705056. ORF7 encodes a protein having the characteristics of a nucleotide sugar epimerase involved in colanic acid biosynthesis.

[D94] - The location of ORF8 is comprised between nucleotide at position nt 1705056 and nucleotide at position nt1705784.

[D95] - The location of ORF9 is comprised between nucleotide at position nt 1705808 and nucleotide at position nt1706593. ORF9 encodes a protein having the characteristics of colanic acid biosynthesis glycosyl transferase.

[096] - The location of ORF10 is comprised between nucleotide at position nt 1706631 and nucleotide at position nt1707524.

[097] - The location of ORF11 is comprised between nucleotide at position nt 1707530 and nucleotide at position nt1708648. ORF11 encodes a protein similar to a spore 5 coat polysaccharide biosynthesis.

[098] A polynucleotide of interest obtained by the above-disclosed method according to the invention may also contain at least one ORF that encodes all or part of acidic, glycine-rich proteins, belonging to the PE and PPE families, whose genes are often clustered and based on multiple copies of the polymorphic repetitive sequences. The names PE and PPE derive from the fact that the motifs ProGlu (PE, positions 8, 9) and ProProGlu (PPE, positions 7 to 9) are found near the N-terminus in almost all cases. The PE protein family all have a highly conserved N-terminal domain of ~110 amino acid residues, that is predicted to have a globular structure, followed by a C-terminal segment which varies in size, 10 sequence and repeat copy number. Phylogenetic analysis separated the PE family into several groups, the larger of which is the highly repetitive PGRS class containing 55 members whereas the other groups share very limited sequence 15 similarity in their C-terminal domains. The predicted molecular weights of the PE proteins vary considerably as a few members only contain the ~110 amino acid N-terminal domain while the majority have C-terminal extensions ranging in size 20 from 100 up to >1400 residues. A striking feature of the PGRS proteins is their exceptional glycine content (up to 50%) due to the presence of multiple tandem repetitions of GlyGlyAla or GlyGlyAsn motifs or variations thereof.

[099] Like the PE family, the PPE protein family also has a conserved N-terminal domain that comprises ~180 amino acid residues followed by C-terminal segments that vary considerably in sequence and length. These proteins fall into 25 at least three groups, one of which constitutes the MPTR class characterised by the presence of multiple, tandem copies of the motif AsnXGlyXGlyAsnXGly. ^(SEQ ID NO. 730) The second subgroup contains a characteristic, well-conserved motif around 30 position 350 (GlyXXSerValProXXTrp), ^(SEQ ID NO. 731) whereas the other group contains proteins that are unrelated except for the presence of the common 180-residue PPE domain. C-terminal extensions may range in size from 00 up to 3500 residues.

[100] One member of the PGRS sub-family, the WHO antigen 22T (Abou-Zeid 35 et al., 1991), a 55kD protein capable of binding fibronectin, is produced during

disease and elicits a variable antibody response suggesting either that individuals mount different immune responses or that this PGRS-protein may not be produced in this form by all strains of *M. tuberculosis*. In other words, at least some PE_PGRS coding sequences encode for proteins that are involved in the 5 recognition of *M. tuberculosis* by the immune system of the infected host. Therefore, differences in the PGRS sequences could represent the principal source of antigenic variation in the otherwise genetically and antigenically homogeneous bacterium.

[D101] By performing the method of the invention using the *M. tuberculosis* BAC 10 based DNA library I-1945, the inventors have discovered the occurrence of sequence differences between a given PGRS encoding ORF (ORF reference on the genomic sequence of *M. tuberculosis* Rv0746) of *M. tuberculosis* and its counterpart sequence in the genome of *M. bovis* BCG.

[D102] More precisely, the inventors have determined that one ORF contained in 15 BAC vector N° Rv418 of the *M. tuberculosis* BCG I-1945 DNA library carries both base additions and base deletions when compared with the corresponding ORF in the genome of *M. bovis* BCG that is contained in the BAC vector N° X0175 of the *M. bovis* BCG I-²⁰⁴⁹XXXXDNA libary. The variations observed in the base sequences correspond to variations in the C-terminal part of the aminoacid 20 sequence of the PGRS ORF translation product.

[D103] As shown in Figure 6, an amino acid stretch of 9 residues in length is 25 present in this *M. tuberculosis* PGRS (ORF reference Rv0746) and is absent from the ORF counterpart of *M. bovis* BCG, namely the following amino acid sequence: (SEQ ID NO. 732)

[D104] NH₂-GGAGGAGGSSAGGGGAGGAGGAGGWLLGD-COOH

[D105] Furthermore, Figure 6 shows also that an amino acid stretch of 45 residues in 30 length is absent from this *M. tuberculosis* PGRS and is present in the ORF counterpart of *M. bovis* BCG, namely following amino acid sequence:

[D106] NH₂-GAGGIGGIGGNANGGAGGNGGTGGQLWGSGGAGVEGGAAL

35 SVGDT-COOH (SEQ ID NO. 733)

[D107] Similar observations were made with PPE ORF Rv0442, which showed a 5 codon deletion relative to a *M. bovis* amino acid sequence.

[D108] Given that the polymorphism associated with the PE-PGRS or PEE ORFS 35 resulted in extensive antigenic variability or reduced antigen presentation, this would be of immense significance for vaccine design, for understanding

protective immunity in tuberculosis and, possibly, explain the varied responses seen in different BCG vaccination programmes.

[0109] There are several striking parallels between the PGRS proteins and the Epstein-Barr virus-encoded nuclear antigens (EBNA). Both polypeptide families are glycine-rich, contain Gly-Ala repeats that represent more than one third of the molecule, and display variation in the length of the repeat region between different isolates. The Gly-Ala repeat region of EBNA1 has been shown to function as a *cis*-acting inhibitor of antigen processing and MHC class I-restricted antigen presentation (Levitskaya et al., 1995). The fact that MHC class I knock-out mice are extremely susceptible to *M. tuberculosis* underlines the importance of MHC class I antigen presentation in protection against tuberculosis. Therefore, it is possible that the PE/PPE protein family also play some role in inhibiting antigen presentation, allowing the bacillus to hide from the host's immune system.

[0110] As such the novel and nonobvious PGRS polynucleotide from *M. bovis* which is homolog to the *M. tuberculosis* ORF Rv0746, and which is contained in the BAC clone N° X0175 (See Table 4 for SP6 and T7 end-sequences of clone n° X0175) of the I-[XXXX]²⁰⁴⁹ *M. bovis* BCG BAC DNA library is part of the present invention, as it represents a starting material in order to define specific probes or primers useful for detection of antigenic variability in mycobacterial strains, possible inhibition of antigen processing as well as to differentiate *M. tuberculosis* from *M. bovis* BCG.

[0111] Thus, a further object of the invention consists in a polynucleotide comprising the sequence SEQ ID N°4.

[0112] Polynucleotides of interest have been defined by the inventors as useful detection tools in order to differentiate *M. tuberculosis* from *M. bovis* BCG. Such polynucleotides are contained in the 45 aminoacid length coding sequence that is present in *M. bovis* BCG but absent from *M. tuberculosis*. This polynucleotide has a sequence beginning (5'end) at the nucleotide at position nt 729 of the sequence SEQ ID N°4 and ending (3'end) at the nucleotide in position nt 863 of the sequence SEQ ID N°4.

[0113] Thus, part of the present invention is also a polynucleotide which is chosen among the following group of polynucleotides :

[0114] a) a polynucleotide comprising at least 8 consecutive nucleotides of the 35 nucleotide sequence SEQ ID N°5 ;

[0115] b) a polynucleotide which sequence is fully complementary to the sequence of the polynucleotide defined in a) ;

[0116] c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

5 [0117] The stringent hybridization conditions for the purpose of defining the above disclosed polynucleotide are defined herein before in the specification.

[0118] The invention also provides for a BAC-based *Mycobacterium tuberculosis* strain H37Rv genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes on November 19, 1997 under the 10 accession number I-1945.

[0119] A further object of the invention consists in a recombinant BAC vector which is chosen among the group consisting of the recombinant BAC vectors belonging to the BAC-based DNA library I-1945.

[0120] Generally, a recombinant BAC vector of interest may be chosen among 15 the following set or group of BAC vectors contained in the BAC-based DNA library I-1945 :

[0121] Rv101; Rv102; Rv103; Rv104; Rv105; Rv106; Rv107; Rv108; Rv109; Rv10; Rv110; Rv111; Rv112; Rv113; Rv114; Rv115; Rv116; Rv117; Rv118; Rv119; Rv11; Rv120; Rv121; Rv122; Rv123; Rv124; Rv126; Rv127; Rv128; Rv129;

20 Rv130; Rv132; Rv134; Rv135; Rv136; Rv137; Rv138; Rv139; Rv13; Rv140; Rv141; Rv142; Rv143; Rv144; Rv145; Rv146; Rv147; Rv148; Rv149; Rv14; Rv150; Rv151; Rv152; Rv153; Rv154; Rv155; Rv156; Rv157; Rv159; Rv15; Rv160; Rv161; Rv162; Rv163; Rv164; Rv165; Rv166; Rv167; Rv169; Rv16; Rv170; Rv171; Rv172; Rv173; Rv174; Rv175; Rv176; Rv177; Rv178; Rv179;

25 Rv17; Rv180; Rv181; Rv182; Rv183; Rv184; Rv185; Rv186; Rv187; Rv188; Rv18; Rv190; Rv191; Rv192; Rv193; Rv194; Rv195; Rv196; Rv19; Rv1; Rv201; Rv204; Rv205; Rv207; Rv209; Rv20; Rv214; Rv215; Rv217; Rv218; Rv219; Rv21; Rv220; Rv221; Rv222; Rv223; Rv224; Rv225; Rv226; Rv227; Rv228; Rv229; Rv22; Rv230; Rv231; Rv232; Rv233; Rv234; Rv235; Rv237; Rv240;

30 Rv241; Rv243; Rv244; Rv245; Rv246; Rv247; Rv249; Rv24; Rv251; Rv252; Rv253; Rv254; Rv255; Rv257; Rv258; Rv259; Rv25; Rv260; Rv261; Rv262; Rv263; Rv264; Rv265; Rv266; Rv267; Rv268; Rv269; Rv26; Rv270; Rv271; Rv272; Rv273; Rv274; Rv275; Rv276; Rv277; Rv278; Rv279; Rv27; Rv280; Rv281; Rv282; Rv283; Rv284; Rv285; Rv286; Rv287; Rv288; Rv289; Rv28;

35 Rv290; Rv291; Rv292; Rv293; Rv294; Rv295; Rv296; Rv29; Rv2; Rv301;

Rv302; Rv303; Rv304; Rv306; Rv307; Rv308; Rv309; Rv30; Rv310; Rv311; Rv312; Rv313; Rv314; Rv315; Rv316; Rv317; Rv318; Rv319; Rv31; Rv32; Rv322; Rv327; Rv328; Rv329; Rv32; Rv330; Rv331; Rv333; Rv334; Rv335; Rv336; Rv337; Rv338; Rv339; Rv33; Rv340; Rv341; Rv343; Rv344; Rv346; 5 Rv347; Rv348; Rv349; Rv34; Rv350; Rv351; Rv352; Rv353; Rv354; Rv355; Rv356; Rv357; Rv358; Rv359; Rv35; Rv360; Rv361; Rv363; Rv364; Rv365; Rv366; Rv367; Rv368; Rv369; Rv36; Rv370; Rv371; Rv373; Rv374; Rv375; Rv376; Rv377; Rv378; Rv379; Rv37; Rv381; Rv382; Rv383; Rv384; Rv385; Rv386; Rv387; Rv388; Rv389; Rv38; Rv390; Rv391; Rv392; Rv393; Rv396; 10 Rv39; Rv3; Rv40; Rv412; Rv413; Rv414; Rv415; Rv416; Rv417; Rv418; Rv419; Rv41; Rv42; Rv43; Rv44; Rv45; Rv46; Rv47; Rv48; Rv49; Rv4; Rv50; Rv51; Rv52; Rv53; Rv54; Rv55; Rv56; Rv57; Rv58; Rv59; Rv5; Rv60; Rv61; Rv62; Rv63; Rv64; Rv65; Rv66; Rv67; Rv68; Rv69; Rv6; Rv70; Rv71; Rv72; Rv73; Rv74; Rv75; Rv76; Rv77; Rv78; Rv79; Rv7; Rv80; Rv81; Rv82; Rv83; Rv84; 15 Rv85; Rv86; Rv87; Rv88; Rv89; Rv8; Rv90; Rv91; Rv92; Rv94; Rv95; Rv96; Rv9.

[0122] The end sequences of the polynucleotide inserts of each of the above clones corresponding respectively to the sequences adjacent to the T7 promoter and to the Sp6 promoter on the BAC vector are shown in Table 3.

20 [0123] It has been shown by the inventors that the minimal overlapping set of BAC vectors of the BAC-based DNA library I-1945 contains 68 unique BAC clones and practically spans almost the whole H37Rv chromosome with the exception of a single gap of approximately 150 kb.

[0124] More specifically, a recombinant BAC vector of interest is chosen among 25 the following set or group of BAC vectors from the BAC-based DNA library I-1945, the location of which vector DNA inserts on the chromosome of *M. tuberculosis* is shown in Figure 3 :

[0125] Rv234; Rv351; Rv166; Rv35; Rv415; Rv404; Rv209; Rv272; Rv30; Rv228; Rv233; Rb38; Rv280; Rv177; Rv48; Rv374; Rv151; Rv238; Rv156; Rv92; Rv3; 30 Rv403; Rv322; Rv243; Rv330; Rv285; Rv233; Rv219; Rv416; Rv67; Rv222; Rv149; Rv279; Rv87; Rv273; Rv266; Rv25; Rv136; Rv414; Rv13; Rv289; Rv60; Rv104; Rv5; Rv165; Rv215; Rv329; Rv240; Rv19; Rv74; Rv411; Rv167; Rv56; Rv80; Rv164; Rv59; Rv313; Rv265; Rv308; Rv220; Rv258; Rv339; Rv121; Rv419; Rv418; Rv45; Rv217; Rv134; Rv17; Rv103; Rv21; Rv22; Rv2; Rv270; 35 Rv267; Rv174; Rv257; Rv44; Rv71; Rv7; Rv27; Rv191; Rv230; Rv128; Rv407;

Rv106; Rv39; Rv255; Rv74; Rv355; Rv268; Rv58; Rv173; Rv264; Rv417; Rv401; Rv144; Rv302; Rv81; Rv163; Rv281; Rv221; Rv420; Rv175; Rv86; Rv412; Rv73; Rv269; Rv214; Rv287; Rv42; Rv143.

[0126] The polynucleotides disclosed in Table 3 may be used as probes in order 5 to select a given clone of the BAC DNA library I-1945 for further use.

[0127] The invention also provides for a BAC-based *Mycobacterium bovis* strain Pasteur genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes on [XXXX XX], 1998 under the accession number I-[XXXX] ²⁰⁴⁹ ↗ June 30

10 [0128] A further object of the invention consists in a recombinant BAC vector which is chosen among the group consisting of the recombinant BAC vectors belonging to the BAC-based DNA library I-[XXXX] ²⁰⁴⁹. This DNA library contains approximately 1600 clones. The average insert size is estimated to be ~80 kb.

[0129] Generally, a recombinant BAC vector of interest may be chosen among 15 the following set or group of BAC vectors contained in the BAC-based DNA library I-[XXXX] ²⁰⁴⁹

[0130] X0001; X0002; X0003; X0004; X0006; X0007; X0008; X0009; X0010; X0012; X0013; X0014; X0015; X0016; X0017; X0018; X0019; X0020; X0021; X0175.

[0131] The end sequences of the polynucleotide inserts of each of the above 20 clones corresponding respectively to the sequences adjacent to the T7 promoter and to the Sp6 promoter on the BAC vector are shown in Table 4.

[0132] The polynucleotides disclosed in Table 4 may be used as probes in order to select a given clone of the BAC DNA library I-[XXXX] ²⁰⁴⁹ for further use.

[0133] Are also part of the invention the polynucleotide inserts that are contained 25 in the above described BAC vectors, that are useful as primers or probes.

[0134] These polynucleotides and nucleic acid fragments may be used as primers for use in amplification reactions, or as nucleic probes.

[0135] PCR is described in the US patent N° 4,683,202. The amplified fragments 30 may be identified by an agarose or a polyacrylamide gel electrophoresis, or by a capillary electrophoresis or alternatively by a chromatography technique (gel filtration, hydrophobic chromatography or ion exchange chromatography). The specificity of the amplification may be ensured by a molecular hybridization using, for example, one of the initial primers as nucleic probes.

[0136] Amplified nucleotide fragments are used as probes in hybridization 35 reactions in order to detect the presence of one polynucleotide according to the

present invention or in order to detect mutations in the genome of the given mycobacterium of interest, specifically a mycobacterium belonging to the *Mycobacterium tuberculosis* complex and more specifically *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG.

5 [0137] Are also part of the present invention the amplified nucleic fragments (« amplicons ») defined herein above.

[0138] These probes and amplicons may be radioactively or non-radioactively labeled, using for example enzymes or fluorescent compounds.

10 [0139] Other techniques related to nucleic acid amplification may also be used and are generally preferred to the PCR technique.

[0140] The Strand Displacement Amplification (SDA) technique (Walker et al., 1992) is an isothermal amplification technique based on the ability of a restriction enzyme to cleave one of the strands at his recognition site (which is under a hemiphosphorothioate form) and on the property of a DNA polymerase 15 to initiate the synthesis of a new strand from the 3'OH end generated by the restriction enzyme and on the property of this DNA polymerase to displace the previously synthesized strand being localized downstream. The SDA method comprises two main steps :

[0141] a) The synthesis, in the presence of dCTP-alpha-S, of DNA molecules that are 20 flanked by the restriction sites that may be cleaved by an appropriate enzyme.

[0142] b) The exponential amplification of these DNA molecules modified as such, by enzyme cleavage, strand displacement and copying of the displaced strands. The steps of cleavage, strand displacement and copy are repeated a sufficient number of times in order to obtain an accurate sensitivity of the assay.

25 [0143] The SDA technique was initially realized using the restriction endonuclease HincII but is now generally practised with an endonuclease from *Bacillus stearothermophilus* (BSOBI) and a fragment of a DNA polymerase which is devoid of any 5'→3' exonuclease activity isolated from *Bacillus cladotetanax* (exo- Bca) [=exo-minus-Bca]. Both enzymes are able to operate at 30 60°C and the system is now optimized in order to allow the use of dUTP and the decontamination by UDG. When using this technique, as described by Spargo et al. in 1996, the doubling time of the target DNA is of 26 seconds and the amplification rate is of 10¹⁰ after an incubation time of 15 min at 60°C.

[0144] The SDA amplification technique is more easy to perform than PCR (a single thermostated waterbath device is necessary) and is faster than the other amplification methods.

5 [0145] Thus, another object of the present invention consists in using the nucleic acid fragments according to the invention (primers) in a method of DNA or RNA amplification according to the SDA technique. For performing SDA, two pairs of primers are used : a pair of external primers (B1, B2) consisting of a sequence specific for the target polynucleotide of interest and a pair of internal primers (S1, S2) consisting of a fusion oligonucleotide carrying a site that is recognized 10 by a restriction endonuclease, for example the enzyme BSOBI.

[0146] The operating conditions to perform SDA with such primers are described in Spargo et al, 1996.

15 [0147] The polynucleotides of the invention and their above described fragments, especially the primers according to the invention, are useful as technical means for performing different target nucleic acid amplification methods such as :

[0148] - TAS (Transcription-based Amplification System), described by Kwok et al. in 1989.

[0149] - SR (Self-Sustained Sequence Replication), described by Guatelli et al. in 1990.

[0150] - NASBA (Nucleic acid Sequence Based Amplification), described by Kievitis et 20 al. in 1991.

[0151] - TMA (Transcription Mediated Amplification).

[0152] The polynucleotides according to the invention are also useful as technical means for performing methods for amplification or modification of a nucleic acid used as a probe, such as :

25 [0153] - LCR (Ligase Chain Reaction), described by Landegren et al. in 1988 and improved by Barany et al. in 1991 who employ a thermostable ligase.

[0154] - RCR (Repair Chain Reaction) described by Segev et al. in 1992.

[0155] - CPR (Cycling Probe Reaction), described by Duck et al. in 1990.

[0156] - Q-beta replicase reaction, described by Miele et al. in 1983 and improved by 30 Chu et al. in 1986, Lizardi et al. in 1988 and by Burg et al. and Stone et al. in 1996.

[0157] When the target polynucleotide to be detected is a RNA, for example a mRNA, a reverse transcriptase enzyme will be used before the amplification reaction in order to obtain a cDNA from the RNA contained in the biological 35 sample. The generated cDNA is subsequently used as the nucleic acid target for

the primers or the probes used in an amplification process or a detection process according to the present invention.

[0158] The non-labeled polynucleotides or oligonucleotides of the invention may be directly used as probes. Nevertheless, the polynucleotides or oligonucleotides 5 are generally labeled with a radioactive element (^{32}P , ^{35}S , ^3H , ^{125}I) or by a non-isotopic molecule (for example, biotin, acetylaminofluorene, digoxigenin, 5-bromodesoxyuridin, fluorescein) in order to generate probes that are useful for numerous applications.

[0159] Examples of non-radioactive labeling of nucleic acid fragments are 10 described in the french patent N° FR-7810975 or by Urdea et al. or Sanchez-Pescador et al., 1988.

[0160] In the latter case, other labeling techniques may be also used such as those 15 described in the french patents FR-2 422 956 and 2 518 755. The hybridization step may be performed in different ways (Matthews et al., 1988). The more general method consists of immobilizing the nucleic acid that has been extracted 20 from the biological sample onto a substrate (nitrocellulose, nylon, polystyrene) and then to incubate, in defined conditions, the target nucleic acid with the probe. Subsequently to the hybridization step, the excess amount of the specific probe is discarded and the hybrid molecules formed are detected by an appropriate method (radioactivity, fluorescence or enzyme activity measurement).

[0161] Advantageously, the probes according to the present invention may have 25 structural characteristics such that they allow the signal amplification, such structural characteristics being, for example, branched DNA probes as those described by Urdea et al. in 1991 or in the European patent N° EP-0 225 807 (Chiron).

[0162] In another advantageous embodiment of the probes according to the 30 present invention, the latters may be used as « capture probes », and are for this purpose immobilized on a substrate in order to capture the target nucleic acid contained in a biological sample. The captured target nucleic acid is subsequently detected with a second probe which recognizes a sequence of the target nucleic acid which is different from the sequence recognized by the capture probe.

[0163] The oligonucleotide probes according to the present invention may also be 35 used in a detection device comprising a matrix library of probes immobilized on a substrate, the sequence of each probe of a given length being localized in a shift of one or several bases, one from the other, each probe of the matrix library thus

being complementary to a distinct sequence of the target nucleic acid. Optionally, the substrate of the matrix may be a material able to act as an electron donor, the detection of the matrix positons in which an hybridization has occurred being subsequently determined by an electronic device. Such matrix libraries of probes

5 and methods of specific detection of a targer nucleic acid is described in the European patent application N° EP-0 713 016 (Affymax technologies) and also in the US patent N° US-5,202,231 (Drmanac).

[0164] Since almost the whole length of a mycobacterial chromososome is covered by a BAC-based genomic DNA libraries according to the present invention (i.e. 97% of 10 the *M. tuberculosis* chromosome is covered by the BAC library I-1945), these DNA libraries will play an important role in a plurality of post-genomic applications, such as in mycobacterial gene expression studies where the canonical set of BACs could be used as a matrix for hybridization studies. Probing such matrices with cDNA probes prepared from total mRNA will uncover genetic loci induced or repressed 15 under different physiological conditions (Chuang et al., 1993; Trieselmann et al., 1992). As such, the H37Rv BAC library represents a fundamental resource for present and future genomics investigations.

[0165] The BAC vectors or the polynucleotide inserts contained therein may be directly used as probes, for example when immobilized on a substrate such as 20 described herein before.

[0166] The BAC vectors or their polynucleotide inserts may be directly adsorbed on a nitrocellulose membrane, at predetermined locations on which one or several polynucleotides to be tested are then put to hybridize therewith.

[0167] Preferably, a collection of BAC vectors that spans the whole genome of 25 the mycobacterium under testing will be immobilized, such as, for example, the set of 68 BAC vectors of the I-1945 DNA library that is described elsewhere in the specification and shown in Figure 3.

[0168] The immobilization and hybridization steps may be performed as described in the present Materials and Methods Section.

30 [0169] As another illustrative embodiment of the use of the BAC vectors of the invention as polynucleotide probes, these vectors may be useful to perform a transcriptional activity analysis of mycobacteria growing in different environmental conditions, for example under conditions in which a stress response is expected, as it is the case at an elevated temperature, for example 35 40°C.

[0170] In this specific embodiment of the invention, Genescreen membranes may be used to immobilize the restriction endonuclease digests (*Hind*III digests for the BAC DNA library I-1945) of the BAC vectors by transfer from a gel (Trieselmann et al., 1992).

5 [0171] Alternatively, the BAC vectors may be immobilized for dot blot experiments as follows. First, the DNA concentration of each BAC clone is determined by hybridization of blots of clone DNAs and of a BAC vector concentration standard with a BAC vector specific DNA probe. Hybridization is quantified by the Betascope 603 blot analyzer (Betagen Corp.), which collects 10 beta particles directly from the blot with high efficiency. Then, 0.5 μ g of each clone DNA is incubated in 0.25 M NaOH and 10 mM EDTA at 65°C for 60 min to denature the DNA and degrade residual RNA contaminants. By using a manifold filtration system (21 by 21 wells), each clone DNA is blotted onto a GeneScreen Plus nylon membrane in the alkaline solution. After neutralization, 15 the blots are baked at 85°C for 2 h under vacuum. Positive and negative controls are added when necessary. In order to perform this procedure, it may be referred to the article of Chuang et al. (1993).

[0172] For RNA extractions, cells grown in a suitable volume of culture medium may, for example, be immediately mixed with an equal volume of crushed ice at - 20 70°C and spun at 4°C in a 50 ml centrifugation tube. The cell pellet is then suspended in 0.6 ml of ice-cold buffer (10 mM KCl, 5 mM MgCl₂, 10 mM Tris; pH 7.4) and then immediately added to 0.6 ml of hot lysis buffer (0.4 M NaCl, 40 mM EDTA, 1% beta-mercaptoethanol, 1% SDS, 20 mM Tris; pH 7.4) containing 100 μ l of water saturated phenol. This mixture is incubated in a boiling water 25 bath for 40 s. The debris are removed by centrifugation. The supernatant is extracted with phenol-chloroform five times, ethanol precipitated, and dried. The dried RNA pellet is dissolved in water before use.

[0173] Then labeled total cDNA may be prepared by the following method. The 30 reaction mixture contains 15 μ g of the previously prepared total RNA, 5 μ g of pd(N₆) (random hexamers from Pharmacia Inc.), 0.5 mM dATP, 0.5 mM dGTP and 0.5mM DTTP, 5 μ M dCTP, 100 μ Ci of [α -³²P]dCTP (3,000 Ci/mmol), 50 mM Tris-HCl (pH 8.3), 6 mM MgCl₂, 40 mM KCl, 0.5 U of avian myeloblastosis virus reverse transcriptase (Life Science Inc.) in a total volume of 50 μ l. The reaction is allowed to continue overnight at room temperature. EDTA and NaOH 35 are then added to final concentrations of 50 mM and 0.25 M, respectively, and

the mixture is incubated at 65°C for 30 min to degrade the RNA templates. The cDNA is then ready to use after neutralization by adding HCl and Tris buffer.

[0174] The hybridization step may be performed as described by Chuang et al. (1993) and briefly disclosed hereinafter. The DNA dot blot is hybridized to ³²P-

5 labeled total cDNA in a solution containing 0.1% polyvinylpyrrolidone, 0.1% Ficoll, 0.1% sodium Pp_i, 0.1% bovine serum albumin, 0.5% SDS, 100 mM NaCl, and 0.1 mM sodium citrate, pH 7.2, at 65°C for 2 days and then washed with a solution containing 0.1% SDS, 100 mM NaCl, and 10 mM Na-citrate, pH 7.2.

10 The same dot blot is used for hybridization with both control and experimental cDNAs, with an alkaline probe stripping procedure (soaked twice in 0.25M NaOH-0.75 M NaCl at room temperature, 30 min each, neutralized, and completely dried at 65°C for at least 30 min) between the two hybridizations. Quantification may be done with the Betascope 603 blot analyzer (Betagen Corp.).

15 [0175] As it flows from the above technical teachings, another object of the invention consists in a method for detecting the presence of mycobacteria in a biological sample comprising the steps of :

[0176] a) bringing into contact the recombinant BAC vector or a purified polynucleotide according to the invention with a biological sample ;

[0177] 20 b) detecting the hybrid nucleic acid molecule formed between said purified polynucleotide and the nucleic acid molecules contained within the biological sample.

[0178] The invention further deals with a method for detecting the presence of mycobacteria in a biological sample comprising the steps of :

[0179] 25 a) bringing into contact the recombinant BAC vector or a purified polynucleotide according to the invention that has been immobilized onto a substrate with a biological sample ;

[0180] b) bringing into contact the hybrid nucleic acid molecule formed between said purified polynucleotide and the nucleic acid contained in the biological sample 30 with a labeled recombinant BAC vector or a polynucleotide according to the invention, provided that said polynucleotide and polynucleotide of step a) have non-overlapping sequences.

[0181] Another object of the invention consists in a method for detecting the presence of mycobacteria in a biological sample comprising the steps of :

[0182] a) bringing into contact the nucleic acid molecules contained in the biological sample with a pair of primers according to the invention;

[0183] b) amplifying said nucleic acid molecules;

[0184] c) detecting the nucleic acid fragments that have been amplified, for example by 5 gel electrophoresis or with a labeled polynucleotide according to the invention.

[0185] In one specific embodiment of the above detection and/or amplification methods, said methods comprise an additional step wherein before step a), the nucleic acid molecules of the biological sample have been made available to a hybridization reaction.

[0186] In another specific embodiment of the above detection methods, said methods comprise an additional step, wherein, before the detection step, the nucleic acid molecules that are not hybridized with the immobilized purified polynucleotide are removed.

[0187] Also part of the invention is a kit for detecting mycobacteria in a 15 biological sample comprising :

[0188] a) a recombinant BAC vector or a purified polynucleotide according to the invention;

[0189] b) reagents necessary to perform a nucleic acid hybridization reaction.

[0190] The invention also pertains to a kit for detecting a mycobacteria in a 20 biological sample comprising :

[0191] a) a recombinant BAC vector or a purified polynucleotide according to the invention that is immobilized onto a substrate;

[0192] b) reagents necessary to perform a nucleic acid hybridization reaction;

[0193] c) a purified polynucleotide according to the invention which is radioactively or 25 non-radioactively labeled, provided that said polynucleotide and the polynucleotide of step a) have non-overlapping sequences.

[0194] Moreover, the invention provides for a kit for detecting mycobacteria in a biological sample comprising :

[0195] a) a pair of purified primers according to the invention;

[0196] b) reagents necessary to perform a nucleic acid amplification reaction;

[0197] c) optionally, a purified polynucleotide according to the invention useful as a probe.

[0198] The invention embraces also a method for detecting the presence of a genomic DNA, a cDNA or a mRNA of mycobacteria in a biological sample, 35 comprising the steps of :

[D99] a) bringing into contact the biological sample with a plurality of BAC vectors according to the invention or purified polynucleotides according to the invention, that are immobilized on a substrate;

[D200] b) detecting the hybrid complexes formed.

5 [D201] The invention also provides a kit for detecting the presence of genomic DNA, cDNA or mRNA of a mycobacterium in a biological sample, comprising :

[D202] a) a substrate on which a plurality of BAC vectors according to the invention or purified polynucleotides according to the invention have been immobilized;

[D203] b) optionally, the reagents necessary to perform the hybridization reaction.

10 [D204] Additionally, the recombinant BAC vectors according to the invention and the polynucleotide inserts contained therein may be used for performing detection methods based on « molecular combing ». Said methods consist in methods for aligning macromolecules, especially DNA and are applied to processes for detecting, for measuring intramolecular distance, for separating and/or for 15 assaying a macromolecule, especially DNA in a sample.

[D205] These « molecular combing » methods are simple methods, where the triple line S/A/B (meniscus) resulting from the contact between a solvent A and the surface S and a medium B is caused to move on the said surface S, the said macromolecules (i.e. DNA) having a part, especially an end, anchored on the 20 surface S, the other part, especially the other end, being in solution in the solvent A. These methods are particularly fully described in the PCT Application n° PCT/FR 95/00165 filed on February 11, 1994 (Bensimon et al.).

[D206] When performing the « molecular combing » method with the recombinant BAC vectors according to the inventions or their polynucleotide inserts, the 25 latters may be immobilized (« anchored ») on a suitable substrate and aligned as described in the PCT Application n° PCT/FR 95/00165, the whole teachings of this PCT Application being herein incorporated by reference. Then, polynucleotides to be tested, preferably under the form of radioactively or non 30 radioactively labeled polynucleotides, that may consist of fragments of genomic DNA, cDNA etc. are brought into contact with the previously aligned polynucleotides according to the present invention and then their hybridization position on the aligned DNA molecules is determined using any suitable means including a microscope or a suitable camera device.

[D207] Thus, the present invention is also directed to a method for the detection 35 of the presence of a polynucleotide of mycobacterial origin in a biological sample

and/or for physical mapping of a polynucleotide on a genomic DNA, said method comprising :

[0208] a) aligning at least one polynucleotide contained in a recombinant BAC vector according to the invention on the surface of a substrate;

[0209] 5 b) bringing into contact at least one polynucleotide to be tested with the substrate on which the at least one polynucleotide of step a) has been aligned;

[0210] c) detecting the presence and/or the location of the tested polynucleotide on the at least one aligned polynucleotide of step a).

[0211] The invention finally provides for a kit for performing the above method, 10 comprising :

[0212] a) a substrate whose surface has at least one polynucleotide contained in a recombinant BAC vector according to the invention;

[0213] b) optionally, reagents necessary for labeling DNA;

[0214] c) optionnally, reagents necessary for performing a hybridization reaction.

15 [0215] In conclusion, it may be underlined that the alliance of such BAC-based approaches such as described in the present specification to the advances in comparative genomics by the availability of an increased number of complete genomes, and the rapid increase of well-characterized gene products in the public databases, will allow the one skilled in the art an exhaustive analysis of the 20 mycobacterial genome.

MATERIALS AND METHODS

[0216] 1. **DNA-preparation.** Preparation of *M. tuberculosis* H37Rv DNA in agarose plugs was conducted as previously described (Canard et al., 1989; Philipp et al., 25 1996b). Plugs were stored in 0.2 M EDTA at 4°C and washed 3 times in 0.1% Triton X-100 buffer prior to use.

[0217] 2. **BAC vector preparation.** pBeloBAC11 was kindly provided by Dr. Shizuya, Department of Biology, California Institute of Technology (Pasadena, CA). The preparation followed the description of Woo et al., 1994 (Woo et al., 1994).

[0218] 30 3. **Partial digestion with *Hind*III.** Partial digestion was carried out on plugs, each containing approximately 10 µg of high molecular weight DNA, after three one hour equilibration steps in 50 ml of *Hind*III 1X digestion buffer (Boehringer Mannheim, Mannheim, Germany) plus 0.1% Triton X-100. The buffer was then removed and replaced by 1ml/plug of ice-cold *Hind*III enzyme buffer containing 35 20 units of *Hind*III (Boehringer). After two hours incubation on ice, the plugs

were transferred to a 37°C water bath for 30 minutes. Digestions were stopped by adding 500 µl of 50 mM EDTA (pH 8.0).

[0219] 4. **Size selection.** The partially digested DNA was subjected to contour-clamped homogenous electric field (CHEF) electrophoresis on a 1% agarose gel using a 5 BioRad DR III apparatus (BioRad, Hercules, CA) in 1X TAE buffer at 13°C, with a ramp from 3 to 15 seconds at 6 V/cm for 16 hours. Agarose slices from 25 to 75 kb, 75 to 120 kb and 120 to 180 kb were excised from the gel and stored in TE at 4°C.

[0220] 5. **Ligation and transformation.** Agarose-slices containing fractions from 25 to 10 75 kb, 75 to 120 kb and 120 to 180 kb were melted at 65°C for 10 minutes and digested with Gelase (Epicentre Technologies, Madison, WI), using 1 unit per 100 µl gel-slice. 25-100 ng of the size-selected DNA was then ligated to 10 ng of 15 *Hind*III digested, dephosphorylated pBeloBAC11 in a 1:10 molar ratio using 10 units of T4 DNA ligase (New England Biolabs, Beverly, MA) at 16°C for 20 hours. Ligation mixtures were heated at 65°C for 15 minutes, then drop-dialysed against TE using Millipore VS 0.025 mM membranes (Millipore, Bedford, MA). Fresh electrocompetent *E. coli* DH10B cells (Sheng et al., 1995) were harvested from 200 ml of a mid-log (OD₅₅₀=0.5) culture grown in SOB medium. Cells were washed three times in ice-cold water, and finally resuspended in ice-cold 20 water to a cell density of 10¹¹ cells/ml (OD₅₅₀=150). 1 µl of the ligation-mix was used for electroporation of 30 µl of electrocompetent DH10B *E. coli* using a Eurogentec Easyject Plus electroporator (Eurogentec, Seraing, Belgium), with settings of 2.5 kV, 25 µF, and 99 Ω, in 2 mm wide electroporation cuvettes. After 25 electroporation, cells were resuspended in 600 µl of SOC medium, allowed to recover for 45 minutes at 37°C with gentle shaking, and then plated on LB agar containing 12.5 µg/ml chloramphenicol (CM), 50 µg/ml X-gal, and 25 µg/ml IPTG. The plates were incubated overnight and recombinants (white colonies) 30 were picked manually to 96 well plates. Each clone was inoculated 3 times (2 X 200 µl and 1 X 100 µl of 2YT/12.5 µg/ml CM per clone) and incubated overnight. One of the microtiter plates, containing 100 µl culture per well, was maintained as a master plate at -80°C after 100 µl of 80% glycerol were added 35 to each well, while minipreps (Sambrook et al., 1989) were prepared from the remaining two plates to check for the presence of inserts. Clones containing inserts were then designated "Rv" clones, repicked from the master plate to a second set of plates for storage of the library at -80°C.

[0221] 6. Preparation of DNA for sizing, direct sequencing and comparative genomics. A modified Birnboim and Doly protocol (Birnboim et al., 1979) was used for extraction of plasmid DNA for sequencing purposes. Each Rv clone was inoculated into a 50 ml Falcon polypropylene tube containing 40 ml of 2YT medium with 12.5 µg/ml of CM and grown overnight at 37°C with shaking. Cells were harvested by centrifugation and stored at -20°C. The frozen pellet was resuspended in 4 ml of Solution A (50 mM glucose, 10 mM EDTA, 25 mM Tris, pH 8.0) and 4 ml of freshly prepared solution B (0.2 M NaOH, 0.2% SDS) was then added. The solution was gently mixed and kept at room temperature for 5 minutes before adding 4 ml of ice-cold solution C (3M Sodium Acetate, pH 4.7). Tubes were kept on ice for 15 min, and centrifuged at 10,000 rpm for 15 min. After isopropanol precipitation, the DNA pellet was dissolved in 600 µl RNase solution (15 mM Tris HCl pH 8.0, 10 µg/ml RNase A). After 30 minutes at 37°C the DNA solution was extracted with chloroform:isoamylalcohol (24:1) and precipitated from the aqueous phase using isopropanol. The DNA pellet was then rinsed with 70% ethanol, air-dried and dissolved in 30 µl distilled water. In general, DNA prepared by this method was clean and concentrated enough to give good quality results by automatic sequencing (at least 300 bp of sequence). For a few DNA preparations, an additional polyethylene glycol (PEG) precipitation step was necessary, which was performed as follows. The 30 µl of DNA solution were diluted to 64 µl, mixed gently and precipitated using 16 µl 4M NaCl and 80 µl of 13% PEG 8000. After 30 min on ice the tubes were centrifuged at 4°C, the pellet carefully rinsed with 70% ethanol, air-dried and diluted in 20 µl of distilled water.

[0222] 25 7. Sizing of inserts. Insert sizes were determined by pulsed-field gel electrophoresis (PFGE) after cleavage with *Dra*I (Promega). 100-200 ng of DNA was *Dra*I-cleaved in 20 µl total reaction volume, following the manufacturer's recommendations, then loaded onto a 1% agarose gel and migrated using a pulse of 4 s for 15 h at 6.25 V/cm at 10°C on an LKB-Pharmacia CHEF apparatus. 30 Mid-range and low-range PFGE markers (New England Biolabs) were used as size standards. Insert sizes were estimated after ethidium bromide staining of gels.

[0223] 8. Direct sequencing. For each sequencing reaction 7 µl BAC DNA (300-500ng), 2 µl primer (2 µM), 8 µl reaction mix of the *Taq* DyeDeoxy Terminator cycle sequencing kit (Applied Biosystems) and 3 µl distilled water were used.

[0224] After 26 cycles (96°C for 30 sec; 56°C for 15 sec; 60°C for 4 min) in a thermocycler (MJ-research Inc., Watertown, MA) DNA was precipitated using 70 µl of 70% ethanol/0.5 mM MgCl₂, centrifuged, rinsed with 70% ethanol, dried and dissolved in 2 µl of formamide/EDTA buffer. SP6 and T7 samples of 5 32 BAC clones were loaded onto 64 lane, 6% polyacrylamide gels and electrophoresis was performed on a Model 373A automatic DNA sequencer (Applied Biosystems) for 12 to 16 hours. The sequences of oligonucleotides used as primers are shown in Table 1.

[0225] 9. **DOP-PCR.** As an alternate procedure we used partially degenerate 10 oligonucleotides in combination with vector-specific (SP6 or T7) primers to amplify insert ends of BAC clones, following a previously published protocol for P1 clones (Liu et al., 1995). The degenerate primers Deg2, Deg3, Deg4, Deg6 (Table 1) gave the best results for selected amplification of insert termini.

[0226] 15 **Table 1:** Primers used for PCRs and sequencing

[0227] Vector specific Primers for DOP PCR- first amplification step:

[0228] SP6-BAC1: AGT TAG CTC ACT CAT TAG GCA (SEQ ID NO. 734)

[0229] T7-BAC1 : GGA TGT GCT GCA AGG CGA TTA (SEQ ID NO. 735)

[0230] Vector specific Primers (direct sequencing, nested primer for second PCR step)

[0231] 20 SP6 Mid: AAA CAG CTA TGA CCA TGA TTA CGC CAA (SEQ ID NO. 736)

[0232] T7-Belo2: TCC TCT AGA GTC GAC CTG CAG GCA (SEQ ID NO. 737)

[0233] Degenerate Primers:

[0234] Deg2: TCT AGA NNN NNN TCC GGC (SEQ ID NO. 738)

[0235] Deg3: TCT AGA NNN NNN GGG CCC (SEQ ID NO. 739)

[0236] 25 Deg4: CGT TTA AAN NNN NWA GGC CG (SEQ ID NO. 740)

[0237] Deg6: GGT ACT AGT NNN NNW TCC GGC (SEQ ID NO. 741)

[0238] Primers used for the amplification of *M. bovis* DNA in polymorphic chromosomal region of Rv58:

[0239] Primer 1: ACG ACC TCA TAT TCC GAA TCC C (SEQ ID NO. 742)

[0240] 30 Primer 2: GCA TCT GTT GAG TAC GCA CTT CC (SEQ ID NO. 743)

[0241] 10. **Screening by pooled PCR.** To identify particular clones in the library which could not be detected by random end-sequencing of the 400 BAC clones, PCR-screening of DNA pools was performed. Primers were designed for regions of the 35 chromosome where no BAC coverage was [apparent] using cosmid-or H37Rv ^{apparent}

whole genome shotgun sequences. Primers were designed to amplify approximately 400-500 bp. Ninety-six-well plates containing 200 μ l 2YT/12.5 μ g/ml CM per well were inoculated with 5 μ l of -80°C glycerol stock cultures each from the master plates and incubated overnight. The 96 clones of each plate were pooled by taking 20 μ l of culture from each well and this procedure was repeated for 31 plates. Pooled cultures were centrifuged, the pellets were resuspended in sterile water, boiled for 5 minutes, centrifuged and the supernatants kept for PCRs. As an initial screening step, the 31 pools of a total of 2976 BACs, representing about two thirds of the library were tested for the presence of a specific clone using appropriate PCR primers. PCR was performed using 10 μ l of supernatant, 5 μ l of assay buffer (100 mM b-mercaptoethanol, 600 mM Tris HCl (pH 8.8), 20 mM MgCl₂, 170 mM (NH₄)₂SO₄), 5 μ l of Dimethylsulfoxide (DMSO), 5 μ l of dNTPs (20 mM), 5 μ l of water, 10 μ l primer (2 μ M), 10 μ l inverse primer (2 μ M) and 0.2 units of *Taq* DNA polymerase (Boehringer). 32 cycles of PCR (95°C for 30 s, 55°C for 1 min 30 s, 72°C for 2 min) were performed after an initial denaturation at 95°C for 1 min. An extension step at 72 °C for 5 min finished the PCR. If a pool of 96 clones yielded an appropriate PCR product (Fig. 1A), subpools were made to identify the specific clone. Subpools representative for lane A of a 96 well plate were made by pooling clones 1 to 12 from lane A into a separate tube. Subpools for lanes B to H were made in the same way. In addition, subpools of each of the 12 rows (containing 8 clones each) were made, so that for one 96 well plate, 20 subpools were obtained. PCR with these 20 subpools identified the specific clone (Fig. 1B, lower gel portion). If more than one specific clone was present among the 96 clones of one plate (Fig. 1B, upper gel portion), additional PCR reactions had to be performed with the possible candidates (data not shown).

[0242] 11. **Genomic comparisons.** DNA from the BAC clone Rv58 was digested with the restriction endonucleases *Eco*RI and *Pvu*II, and resolved by agarose gel electrophoresis at low voltage overnight (1.5 V/cm). DNA was transferred via the method of Southern to nitrocellulose membranes (Hybond C extra, Amersham) following standard protocols (Sambrook et al., 1989), then fixed to the membranes at 80°C for 2 hours. The blot was hybridized with ³²P labelled total genomic DNA from *M. tuberculosis* H37Rv, *M. bovis* type strain (ATCC 19210) or *M. bovis* BCG Pasteur. Hybridization was performed at 37°C overnight in

50% formamide hybridization buffer as previously described (Philipp et al., 1996b). Results were interpreted from the autoradiograms.

[D243] 12. **Computer analysis.** Sequence data from the automated sequencer ABI373A were transferred as binary data to a Digital Alpha 200 station or Sun SparcII station and analysed using TED, a sequence analysis program from the Staden software package (Dear et al., 1991). Proof-read sequences were compared using the BLAST programs (Altschul et al., 1990) to the *M. tuberculosis* H37Rv sequence databases of the Sanger Centre, containing the collected cosmid sequences (TB.dbs) and whole-genome shotgun reads (TB_shotgun_all.dbs) (<http://www.sanger.ac.uk/>). In addition, local databases containing 1520 cosmid end-sequences and the accumulating BAC end-sequences were used to determine the exact location of end-sequenced BACs on the physical and genetic map. MycDB (Bergh et al., 1994) and public databases (EMBL, Genbank) were also used to compare new sequences, but to a lesser extent. The organization of the open reading frames (ORFs) in the polymorphic region of clone Rv58 was determined using the DIANA software established at the Sanger Centre.

EXAMPLES

[D244] Example 1 : Construction of a pBeloBAC11 library of *M. tuberculosis* H37Rv.

[D245] Partial *Hind*III fragments of H37Rv DNA in the size range of 25 to 180 kb were ligated into pBeloBAC11 and electroporated into strain *E. coli* DH10B. While cloning of fractions I (25 to 75 kb) and II (75 to 120 kb) gave approximately 4×10^4 transformants (white colonies), cloning of fraction III (120 to 180 kb) repeatedly resulted in empty clones. Parallel cloning experiments using partial *Hind*III digests of human DNA resulted in stable inserts for all three fractions (data not shown), suggesting that the maximum size of large inserts in BAC clones is strongly dependent on the source of the DNA. Analysis of the clones for the presence of inserts revealed that 70 % of the clones had an insert of the appropriate size while the remaining 30% of white colonies represented empty or *lacZ*'-mutated clones. Size determination of randomly selected, *Dra*I-cleaved BACs via PFGE showed that the insert sizes ranged for the majority of the clones between 40 kb and 100 kb with an average size of 70 kb. Clones with inserts of appropriate size were designated with "Rv" numbers, recultured and stored at -80°C for further use.

[D246] Example 2 : Direct DNA sequence analysis of BACs.

[D247] To characterize the BAC clones, they were systematically subjected to insert termini sequencing. Two approaches, direct sequencing of BAC DNA and PCR with degenerate oligonucleotide primers (DOP), adapted to the high G+C content of mycobacterial DNA, were used. In a first screening phase, 50 BAC clones designated Rv1 to Rv50 were analysed using both methods in parallel. Except for two clones, where the sequences diverged significantly, the sequences obtained by the two methods only differed in length. Sequences obtained directly were on average about 350 bp long and for 95% of the clones both the SP6 and T7 end-sequences were obtained at the first attempt. Sequences obtained by DOP-PCR were mostly shorter than 300 bp. For 40% of the BACs we obtained only very short amplicons of 50 to 100 base pairs from one end. In two cases the sequence obtained with the DOP-PCR differed from the sequences obtained by direct sequencing, and in these cases *E.coli* or vector sequences were amplified (data not shown). Taking the advantages and disadvantages of both methods into account, we decided to use direct termini sequencing for the systematic determination of the SP6 and T7 end-sequences.

[D248] Example 3 : Representativity of the library.

[D249] After having determined the end-sequences of 400 BACs a certain redundancy was seen. The majority of clones were represented at least 3 to 4 times. Maximum redundancy was seen in the vicinity of the unique *rrn* operon, as 2.5 % of the clones carried identical fragments that bridge the cosmids Y50 and Y130 (Fig. 3, approximate position at 1440 kb). The majority of clones with identical inserts appeared as two variants, corresponding to both possible orientations of the *Hind*III fragment in pBeloBAC11. This suggests that the redundancy was not the result of amplification during library construction, but due to the limited number of possible combinations of partial *Hind*III fragments in the given size-range of 25 to 120 kb. To detect rare BAC clones, a pooled PCR protocol was used. Primers were designed on the basis of the existing cosmid sequences and used to screen 31 pools of 96 BAC clones. When positive PCR products of the correct size were obtained, smaller subpools (of 8 or 12 clones each) of the corresponding pool were subsequently used to identify the corresponding clone (Figs. 1A and 1B). With this approach 20 additional BACs (Rv401-Rv420) were found for the regions where no BACs were found with the initial systematic sequencing approach. The end-sequences of these BACs

(Rv401-420) were determined by direct sequencing, which confirmed the predicted location of the clones on the chromosome. A 97% coverage of the genome of H37Rv with BAC clones was obtained. Only one region of ~ 150 kb was apparently not represented in the BAC library as screening of all pools with 5 several sets of specific primers did not reveal the corresponding clone. This was probably due to the fact that *Hind*III fragments of mycobacterial DNA larger than 110 kb are very difficult to establish in *E. coli* and that a *Hind*III fragment of ~120 kb is present in this region of the chromosome (data not shown).

[0250] Example 4 : Establishing a BAC map.

10 [0251] Using all end-sequence and shotgun-sequence data from the H37Rv genome sequencing project, most of the BAC clones could then be localized by sequence comparison on the integrated map of the chromosome of *M. tuberculosis* strain H37Rv (Philipp et al., 1996b) and an ordered physical map of the BAC-clones was established. PCR with primers from the termini sequences 15 of selected BACs were used for chromosomal walking and confirmation of overlapping BACs (data not shown). The correct order of BACs on the map was also confirmed more recently, using 40,000 whole genome shotgun reads established at the Sanger Centre. In addition, pulsed-field gel electrophoresis of *Dra*I digests of selected BACs was performed (Fig. 2) in order to see if the 20 approximate fragment size and the presence or absence of *Dra*I cleavage sites in the insert were consistent with the location of the BACs on the physical map (Fig. 3). Comparison of the sequence-based BAC-map with the physical and genetic map, established by PFGE and hybridization experiments (Philipp et al., 1996b), showed that the two maps were in good agreement. The positions of 25 genetic markers previously shown on the physical and genetic map were directly confirmed by BAC-end-sequence data (Table 2, Fig. 3). The position of 43 from 47 Y-clones (91%) shown on the physical and genetic map, which were later shotgun sequenced, was confirmed by the BAC end-sequences and shotgun sequence data. Four clones (Y63, Y180, Y251, and Y253) were located to 30 different positions than previously thought and this was found to be due to book keeping errors or to chimeric inserts. Their present approximate location relative to the *oriC* is shown in Figure 3: Y63 at 380 kb, Y63A at 2300 kb, Y180 at 2160 kb, Y251 at 100 kb, and Y253 at 2700 kb. A total of 48 BACs, covering 35 regions of the chromosome, not represented by cosmids were then shotgun sequenced (Cole et al., 1997), and these are squared in Fig. 3. No chimeric BACs

were found, which is consistent with the observations of other research groups for other BAC libraries (Cai et al., 1995; Zimmer et al., 1997). The absence of chimeric BACs was of particular importance for the correct assembly of the *M. tuberculosis* H37Rv sequence. The exact position of the BAC termini sequences 5 on the chromosome will be available via the world wide web (<http://www.pasteur.fr/MycDB>).

[0252] Table 2 : Identities of genetic markers previously shown on the integrated and genetic map of H37Rv (Phlipp et al., 1996b) [which] showed perfect sequence 10 homology with BAC[en] sequences.

Locus	BAC end sequence	Description of genetic marker	Organism	GenBank Accession n°
<i>apa</i>	Rv163SP6	Secreted alanine-proline-rich antigen	<i>M. tuberculosis</i>	X80268
<i>dnaJ, dnaK</i>	Rv164T7	DnaJ hsp	<i>M. leprae</i>	M95576
<i>fop-A</i>	Rv136T7	Fibronectin binding protein	<i>M. tuberculosis</i>	M27016
<i>polA</i>	Rv401T7	DNA polymerase I	<i>M. tuberculosis</i>	L11920
<i>ponA</i>	Rv273T7	Penicillin binding protein	<i>M. leprae</i>	S82044
<i>psrC</i>	Rv103T7	Putative phosphate transport receptor	<i>M. tuberculosis</i>	Z48057
<i>recA</i>	Rv415SP6	Homologous recombination	<i>M. tuberculosis</i>	X58485
<i>wag9</i>	Rv35SP6	35-kDa antigen	<i>M. tuberculosis</i>	M69187

[0253] Example 5 : Repetitive end-sequences.

[0254] Repetitive sequences can seriously confound mapping and sequence 15 assembly. In the case of the BAC end-sequences, no particular problems with repetitive sequences were observed. Although nine clones with one end in an *IS1081* (Collins et al., 1991) sequence were identified, it was possible to correctly locate their position on the map using the sequence of the second terminus. Moreover, these BACs were used to determine the exact locations of 20 *IS1081* sequences on the map. Five copies of this insertion sequence, which

harbors a *Hind*III cleavage site, were mapped on the previous physical and genetic map. In contrast, BAC end-sequence data revealed an additional copy of *IS1081* on the *M. tuberculosis* H37Rv chromosome. The additional copy was identified by six clones (Rv27, Rv118, Rv142, Rv160, Rv190, Rv371) which 5 harbored an identical fragment linking Y50 to I364 (Fig. 3, at ~ 1380 kb). This copy of *IS1081* was not found by previous hybridization experiments probably because it is located near another copy of *IS1081*, localized on the same *Dra*I fragment Z7 and *Asn*I fragment U (Fig. 3, at ~ 1140 kb). Furthermore, the 10 position of a copy of *IS1081* previously shown in *Dra*I fragment Y1 (Fig. 3, at ~ 1840 kb) had to be changed to the region of Y349 (Fig. 3, at ~ 3340 kb) according to the end-sequences of BAC Rv223. The positions of the four other *IS1081* copies were confirmed by the sequence data and therefore remained unchanged. In total 6 copies of *IS1081* were identified in the H37Rv genome in agreement with the findings of others (Collins et al., 1991).

15 [0255] In addition, a sequence of 1165 bp in length containing a *Hind*III site was found in two copies in the genome of H37Rv in different regions. The end-sequences of BAC clones Rv48 and Rv374, covering cosmid Y164, as well as Rv419 and Rv45, that cover cosmid Y92, had perfect identity with the corresponding parts of this 1165 bp sequence (Fig. 3, at ~ 3480 kb and ~ 900 kb). 20 Analysis of the sequence did not reveal any homology with insertion sequences or other repetitive elements. However, as each of the two locations showed appropriate BAC coverage, chimerism of the sequenced cosmids Y164 and Y92 can be ruled out as the probable cause.

[0256] **Example 6 : Using BAC clones in comparative genomics.**

25 [0257] The minimal overlapping set of BAC clones represents a powerful tool for comparative genomics. For example, with each BAC clone containing on average an insert of 70 kb, it should be possible to cover a 1Mb section of the chromosome with 15 BAC clones. Restriction digests of overlapping clones can then be blotted to membranes, and probed with radiolabelled total genomic DNA 30 from, for example, *M. bovis* BCG Pasteur. Restriction fragments that fail to hybridize with the *M. bovis* BCG Pasteur DNA must be absent from its genome, hence identifying polymorphic regions between *M. bovis* BCG Pasteur and *M. tuberculosis* H37Rv. The results of such an analysis with clone Rv58 (Fig. 3, at ~1680 kb) are shown here. This clone covers a previously described polymorphic 35 genomic region between *M. tuberculosis* and *M. bovis* BCG strains (Philipp et

al., 1996a). *Eco*RI and *Pvu*II digests from clone Rv58, fixed on nitrocellulose membranes, were hybridized with ^{32}P -labelled total genomic DNA from *M. tuberculosis* H37Rv, *M. bovis* (ATCC 19120), and *M. bovis* BCG Pasteur. Figures 4A and 4B present the results of this analysis, where it is clear that several restriction fragments from clone Rv58 failed to hybridize with genomic DNA from either *M. bovis* or *M. bovis* BCG Pasteur. On the basis of the various missing restriction fragments, a restriction map of the polymorphic region was established and compared to the H37Rv sequence data. The localization of the polymorphism could therefore be estimated, and appropriate oligonucleotide primers (Table 1) were selected for the amplification and sequencing of the corresponding region in *M. bovis*. The alignment of *M. bovis* and *M. tuberculosis* H37Rv sequences showed that 12,732 bp were absent from the chromosomal region of the *M. bovis* type strain and *M. bovis* BCG Pasteur strain. The G+C content of the polymorphic region is 62.3 mol%, which is the same as the average genome G+C content of the *M. tuberculosis* genome, hence indicating that this region is not a prophage or other such insertion. Subsequent PCR studies revealed that this segment was also absent from the Danish, Russian, and Glaxo substrains of *M. bovis* BCG, suggesting that this polymorphism can be used to distinguish *M. bovis* from *M. tuberculosis*. Analysis of this sequence showed that 11 putative open reading frames (ORFs) are present in *M. tuberculosis*, corresponding to ORFs MTCY277.28 to MTCY277.38 / accession number Z79701 -EMBL Nucleotide Sequence Data Library (Fig. 5). FASTA searches against the protein and nucleic acid databases revealed that the genes of this region may be involved in polysaccharide biosynthesis. Among these putative genes, the highest score was seen with ORF 6 (MTCY277.33), whose putative product shows a 51.9% identity with GDP-D-Mannose dehydratase from *Pseudomonas aeruginosa* (accession number U18320 - EMBL Nucleotide Sequence Data Library) in a 320 amino acid overlap. The novel *M. bovis* sequence of the polymorphic region was deposited under accession number AJ003103 in the EMBL Nucleotide Sequence Data Library.

[0258] As it appears from the teachings of the specification, the invention is not limited in scope to one or several of the above detailed embodiments; the present invention also embraces all the alternatives that can be performed by one skilled in the same technical field, without deviating from the subject or from the scope of the instant invention.

Table 3 : End-sequences of the polynucleotide inserts cloned in the named recombinant BAC vectors contained in the I-1945 *M. tuberculosis* H37Rv genomic DNA library.

RvXXXSP6 corresponds to the SP6 end-sequence of the clone RvXXX.

RvXXXT7 corresponds to the T7 end-sequence of the clone RvXXX.

RvXXXIS 1081 corresponds to a region located close to a copy of the IS1081 repetitive sequence (Insertion element).

The character « - » denotes an uncertain base residue.

Clone Rv101

: : : : : Rv101SP6.seq: : : : : :

AATACTCAAGCTTGCAGCCGATGACAAGAAATATGTCGGCAAAAGACTCAGCGGCCGACTTTGCTCGCAGCTG
GCGGTACCGCGCCACCGATTCTATGCCGTGGTCGCGGAAAAATGCCTCCGAAATCGCACGGCGACTCCAGTCGG
GAGCATTCCCGATGCCAGCTGCCGTGCCCTGCCGGCACGGCACCCACATGCCAGTTCGTCCACCTGGGCCAG
CGCCCCGCCGAATTCAAACAATAGAACTGCACCCGGCCGCATCGTGGTAACAGCCAACGCCATGATCAGCGT
CCGCAGCGCGGTTGACTTGCCTGGTGCACCTACGAACCGACATTGCCTGCCGGCCGACAAGTCGATCGT
GCGCGCACCCGTGACTGCTCTAACGGCGATTGAAATTCCGAT (SEQ ID N° 6)

: : : : : Rv101T7.seq: : : : : :

CCACCCGTGTAATTGGGATGGGCAAAAAGCGAAGCACCGCGTGGCACGAACGCCGGAGGGACAATCTGGGGCG
TTAGGGCTTCTCGCGGAAGGCCGAACGTACGGCTTCAACACCTCGCTGCCCTCCGACCGCGAACATTGGG
ATGGCAGCAACCTGCTGGCACCTGGCGGGCGATGATCTGCAGCGTCCGCGGGTAGTCGCCGCCGGCTAC
ACTCTGAAACCGGATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTCCCTACACCGCGATATGTCGCCT
CGCTGCCCGGTGGACCGGT (SEQ ID N° 7)

Clone Rv102

: : : : : Rv102SP6.seq: : : : : :

AATACTCAAGCTTCCGCGATACCGCCATGTCGCGCACATCCAGGACTTCTGGGGGATCCGCTGACAGCGCGGG
ATCCCAAAGTGCAGGATGATCGGGCGCCTACGTCGTGGTACCTCGCTGTAACAACGAAACCGAAGCGTATGACTC
GGTCCACCGGTGCGGACATGGTGGACACCACCGCACGGGTGAAGGCTATGTCACCGGTCCGGCAGC
ACTCAATGCCGACCAGGCCGAGGGCGAGACAAAAGTATCGTAAGGTACCGCGATACCAACATGGTATCGCAGC
AATGTTGCTAGTGTATCGCTCCGTAATTACCGCGGTCT (SEQ ID N° 8)

: : : : : Rv102T7.seq: : : : : :

GTGCCGTTCAACCGAATTGGCTTCGGCCCATCGTGAGGACGGCGTGCAGGCTCAACGACGACGTCGTCGG
GGGACACACCTCGATGCTGCCGCGCATGGACCGCGTCAACGCAAGCAGCTGATCAGACTACAACGCCGCGCGAACGC
TTCCGCGCGGGCGTGAACCGCATCCGTTGACCGGGCGATCGCGGTGATCGTCAACGCGCATGCCACCGGAGCG
ACGGCCAAGCGCGCGTGCACGGTCGCCCGGGCGACGGTGCAGGACAAGTGGTCTGGCGGTCCCGATCGGCCAGAC
GACATCGTGGCGAGATCGCCGGTACGCCGATGAGGTGGT (SEQ ID N° 9)

Clone Rv103

: : : : : Rv103SP6.seq: : : : : :

AATACTCAAGCTTCCGCGAAACGGACACATTGCAATTGATGACAAAATAAAATCATTGATGGTTGAGTCAC
CAGGCCGATCAAGCCTTCGCGAGCCAATTCAATCAAGAGGCCAACGCCGACCAATCAGCCGCCAACGAGGGA
TTCCGTCATTATCAGCAAATACTGCTCTGGGTACACCCAAACAGCGCAATATGGCAAAAACGGTCGCCGTTG
CACGACATTAAATGTCACGGTATTGTAGATTAAGAATACCCAC (SEQ ID N° 10)

: : : : : Rv103T7.seq: : : : : :

TGCTCCGAAACCTGGGGGTGTGCCCTGCTCTGTATGCCGACGGCATACGGACATCCTCCCTGAGACCCGCGTCAAC
CAGGCCACGTGTCATCATAGNGGGTCAACCCGCCAACGGCGACGGCACGCCAGTTGCCGACCGTAAACCTAGTG
CTGTTAGCTTCATTGCTGCGATCAAACAGCTGGTCGCCGTTAGGAACGTGAAACTCAACCGATTGGTGCC
GCCGTAGGTGTCCTGGCTGCCGGTGCCTGGTGTCCCGCTGTTGTAACGACGACAATGTGACCGGGGGAGGTGCA
ACCACTGGCCAGGCGTCGGCAAAGGTCGATTGCCGGGAGAAGAACACTCAAAGCCAGTGGGT (SEQ ID N° 11)

Clone Rv104

:::::::Rv104SP6.seq:::::::
 ATACTCAAGCTTGCAGCGGGCGATGTTGATGACGGAAACCCAGCGACAACCGACGATTGGCGTAGCC
 GCGGAGCGTCTGCTCGATTCCGATCACGTCGGCGCTCGCATCGAGCATGGCGCCGACGGCTAGCAGCGATCCGCC
 GTCGTCGAGGAGCACGACACGAGCCGTACGCCGCCGTAAGCCGCCAGGATTGGCGAAAAACGTTCTACGTG
 GCGGGTGTACTGGGTGCGATGATTGTTGGGTGCGTAGGCCTGCTGCAATCGTCGACATAGATGCCGTGGGCC
 CATCGCTGACAACCTCCGGGTGAGTGGAAATAGCACTGCCGATACCGCGACGTTGCCGAGGCGAACCCGA
 ATA (SEQ ID NO. 12)

:::::::Rv104T7.seq:::::::
 TCCTATGCCCCGAGCANGTATCGAACCGCGGTGACAGATTGCTATCCTGGACCTGACGGTGAGGCTGAAGTT
 TTCCAGGAATTGGCAAATCGGTAAAGAGCTGAAGAATTGGTATGCCGACGAAATCTGCACGCAACGGGGC
 ATATACGCTTCGGGTTTACGAGATGTCGATGGGCCGCTGGAGGCTCACGTCATGGGCCACAAAGGATGTTGTCGG
 CGCGTACCGTCTGCAGCGGGTGTGGCGTTGGTCG (SEQ ID NO. 13)

Clone Rv105

:::::::Rv105SP6.seq:::::::
 ATACTCAAGCTGATTCGCCAACCGACCGTGAGCACCCCGCCAGCCACCGCTGGGTGGCGCCGGGCCGG
 GCGGCCAGGCTGCTCGCTGGTATGGCACGCCACCGCGACACCACCCGGCTGCCTACGCTTAACCATTCCAGGCC
 GAGCTACATCAGCTCGGCCAGTGTTCGGGCCCTTTCCAGGTCGAAGTCTATACCGATATGCCGATCCGCAGC
 CGCCACCCCTGGAGAACAGAACGATGCCCTACTAATGCTGTCTGGGGGGCC (SEQ ID NO. 14)

:::::::Rv105T7.seq:::::::
 GGTAACGCTTCGGTCGAGTCTGCGAGTATGCAATGACGACCGGACCTCGTCGGCATCTCCATAGCCGCCACACCT
 TCAGTTGCTCACCGGAATCCAACCGTAGAAGGTCGGCAGCGCTCGGATTGGTCATGGGATATGCCGCTGGGAC
 GGTCAAGAGCCCTCGGGTCCGGCCAGCACTCCGAGGCTTCGTCGGGGTGGTCGCGACGCGCATGGGCCACCATCGCAT
 TCACCAAGGCTGCGCAATCACCAGCACGTAGACGGTTCTTCCTAAGCAACACCGAAGTTTCAGGACCCGAATGCT
 CGGGAAACATGTCACGGTAGGTCGGTATTCCGGTACCGGCTGA (SEQ ID NO. 15)

Clone Rv106

:::::::Rv106SP6.seq:::::::
 GGCGTCAACGGTGTGGAACCCCGCTAACGAAATTGGTAGGCCTGCAGTCGTGAATCAGGCCGACGCTGTGGCCGCC
 GCGGC (SEQ ID NO. 16)

:::::::Rv106T7.seq:::::::
 GGCTNGCGTACCCGGTACCGGCCGGCCTACACGTCGGGAACTGGAAGCGCAGTAAGCCCTAACCGGCCACCG
 CTTTGGCCCGCGCCGGCGTAGGCGATCGCGGTGGCGACTCGCACCTACCAGGGCTTTC
 AGCTTGTGATCACCGGCCAGCATGGTCGANGATGCAATTGAGACCATATTGAAATTGGTTCATCGGGGGCC
 CGATCCGATGCCCTCCAGTTGCGTAGGCAANCAGGGAGTCNTCGGGATCGATGGCACGGGGTGTCAATGG
 CGGATGGTCCGCTGCCGCCACTGGCTTTGCGGAGAACCGATAGCACCAACCGATCCGCGACGTNG (SEQ ID NO. 17)

Clone Rv107

:::::::Rv107T7D4.seq:::::::
 CGTAATNTCGCAGCACANCCANGACTTCTGGGGGATCNGCTGACAGTGGTNGGATCCAAATTGCGGATGATCGGGCC
 GCCNACGTGTTGTGACCTCNCNGTCACAACNAANCGAANCGTATGACTCGGTCCACGCCGTGCCACATGGTG
 GACACCACCCGCCACCGCNCGGGTGAAGGCTATGTCACCGGCCGAAACACTCAATGCCGACCAGGCCGANGCC
 GGACACNANAGTATCCTAACGTCACCGCGATCACGAGCATGGTATCGNNCAATGTTNCTANTGATCTACGCTCCG
 TAATTACCGCGGTTCTCGTCTGATCATGGTCGANCAGACTCCGGCAATCCGGGATTCACTCGNCTTGCCTCGCC
 ATCACATATTTCAGCTTACATGCAACNAACCTGCTCTCATGGNGATGCCGACACGGACTACCGATATC
 ATGCTCGCCGTTACACAATNCGCCACGCCGAAGACNGGAAACGCTTCTACACAATNTTNCGGGACGCCACTNAA
 CTTGGTTCNGGTTGACATTGCCGCGATGNTGCCCAGCTTGCCGGCTCCCTTA (SEQ ID NO. 18)

Clone Rv108

:::::::Rv108T7D4.seq:::::::
 TGAATTCCGATCCCACAATCTGGTTGAGATACAGGTGCCATACCCCTTACTTCGGCAACGCTGGGGGATTGGC
 CCTGCNGCTGCGAGCANACCATCGACGCCATCGAATTGCCGCAATCTCGTTGAGCAATCCATACCCATCGACATTCC
 GCCGATCGACATCCGGCCTTCNCCTTAAACGG (SEQ ID NO. 19)

Clone Rv109

:::::::Rv109SP6.seq:::::::
 AACAGCTATGACCATGNTTACGCCAAGCTATTAGGTAACACTATANAATACTCAAGCTTTACGGTATCGCGCATC
 ACCTGGTTCATGAACCTGGAAAGCAGCGCANCCTCTTTCGGCCGAAACATGAGCCAGCCTCTCGTCCGGTCNGG
 TGCAAGGTGCTCGGGCAGCTCGGCCGACAGCCGCTGACCCCTGAAACACCAGCTTCATATCCCGCAGAACNACNC
 AGTCCGCTACGTAACCCCTCCGCACTGTCCATGGACAACAGCGCTCTCCACCGACCAGGGCCGGGTGTTGGGTG
 TTCGGCAGCCGGCAGCCAGGTGGTCCACACTGCCGACGGCGCCGAGCCGTTACCGACCAAGCCGCGAACAGT
 CCGCCGATCGCATACTCCAACCGGTTGCCGACTGCAGGTACGCTGGGTACCTCCTNTCNCGCTCGCGAAGTCT
 TGCTCCANACGTCGAGAACGGCAAGGAACACGTTCA (SEQ ID NO. 20)

:::::::Rv109T7.seq:::::::
 GACCGNNCATGTTCCACAATGTGGTGCAGTNCGGNGCTACGTGCCATCNANACACTGGCGCAGGCTATCGCACC
 CGTTATCNGCTACGAACAAATCNCGGTATGCGTTCTTANCATGAGTCGGCAGCGATCATGGTCGACACCCACG
 ACNGAAATACGAGATGCCNTNAGCNTGTCGCCGCGATTATCANGACTGACCTCTGGTACCGGNNNTGTNTG
 GTCGCGATGCCCTGGCGCCGGCGCGTGNCTGTCGGCTCGGATAGCGAAGTCAGCTAATTCTGTGGCAGCTCG
 AAAGGGTCCCTGCCGGTGCCGGTCTTGCACGCAACCATGCNCATGTTACGGTCCCTCGGGTGCCTGGCGCGC
 (SEQ ID NO. 21)

Clone Rv10

:::::::Rv10SP6D2.seq:::::::
 GGGATGGGCGGGCCCGCTAAACTCTCGTGTCCACTAACTCCGGAGGGNCAATCTCGGGCGTTATGGCTCACGTC
 CGCTCGCCCTCCGACCGCGAACATTGGAGTTGGCAGCAACCTGGTAGCACCCCTGGCGG (SEQ ID NO. 22)

:::::::Rv10T7D4.seq:::::::
 NCCGTGTTGACAAGTAAATATGTCCGCAAAAGTCTCAGCGGCCGACTTGTCTCGCAGGTGGCGTACCGGCCACCG
 AGTCGATGCCGTGGTCGCCGAGAACATGCCCTCCGAAATCGCACGGCCTTCCNNTAACGGA (SEQ ID NO. 23)

Clone Rv110

:::::::Rv110SP6.seq:::::::
 TTAGGTGACACTATAGAATACTCAAGCTTTGGCTAGCCGGCGAGCAGATACTGGGTGTCAATTGGCACCGCG
 CGGCTGTCCGGAAATGGCGGGTCCCCGGTGGTTTGCTGATGAGTGTGAACCGTANTCGAAGTGGCGCGTCAGA
 CTCCACCCANCCAGCAGCGCAAGCTGAATCCTCCAACCGGGTTGTCNATCCGACAAGTTGGGGTGCCTTGG
 GGAATGACAGGGTGGCNGCGGTGCGTTCGGGTCGCCGGCGGAAGTGTGCTGGATCNCCGCTGGGCATTCGGC
 NTTTTGCGCCGGCCGGTGGTNGGGGGCAACAGGTNTCCNGTGCGGGTGGCGCTAACGGTCACGGCAGGCC
 CGCTTGTGGTACCNGGGCGTGGCTCCGATCGCCTGGCGTNC (SEQ ID NO. 24)

:::::::Rv110T7.seq:::::::
 CTACACCCTGAATACGACGGCGTCGCCNACTTCCGGTACCCGCTCAACTTGTGTCGACCCCTAACGCCATTGC
 CGGCACCTACTACGTGCACTCCAACACTTCATCCTGACGCCGAACAAATTGACGAGCGGTTCCGCTGACCAATAC
 GGTGGTCCCACGATGACCCAGTACTACATCATTGCAACGGAAACCTGCGCTGCTAGAGCACTGCGATCGGTGCC
 GATCGTGGGAAACCCACTGGCAACCTGGTCAACCAAACCTGAANGTGAATTGTTAACCTGGCTACNGCACC
 CTATGGTTATTACNACCTNCCGCCAATGTTGCGACTCCGGTTGTTCCANAAGTCNNCCGGTGTACCGC
 CGAACANCTCTCCGGGACCCACAGGGAAATCNGCNATTNCCTACAAATCANCACCTCCA (SEQ ID NO. 25)

Clone Rv111

:::::::Rv111T7.seq:::::::
 GCATGATCGGGCACCTTCGGCCGCCGGCATACGGCGGCTACCGATCTCCGGTACATACACCCGGTAATCGC
 CGACGGTGCCTCGCGAGCGAAGGTGACGACTCTGATTGAATCGAGTTCCAGGTCCAGGGTGGCGACCAACG
 CGCGAGCTAACGACGTCATCNGTTGCGCTTCTACGGTACCCGACCCCTGGTACCGTAGTTNC (SEQ ID NO. 26)

Clone Rv112

:::::::Rv112SP6.seq:::::::
 GACACTATAGAATACTCAAGCTTGCACCGCAGCGCTGCATCCGGCGGANCAGTGTCCGGCGACCAGTACGAAC
 CAACCTCGGGTGCCTGGGCCATTGACGATGTGCTGGTGGCGCCCGAGTCGCGCACCACGCGCGGGCACC
 ACCANGCGGGCCCACCCCTGCACGGGACGATCATTCCGGCGCCGCTACGGCGGGGGCTGAACANGCACAGCA
 TCAACGTNGTACCCGGCGTACGGGCCGACCGGGCCGACCGTACACACCACCAAGCCATTGCGTCTCCTCAACNGGGCGA
 CCCGGCCGACCGTACACGGNCTAAGGCCATTGCCGTCTCCT (SEQ ID NO. 27)

:::::::Rv112T7.seq:::::::

PCT/IB99/00740

(SEQ ID NO. 29)

TCGGGCCATCGGCACCTTCGAGGACCTGTATTCGACGCCGCTGGCCNACCTGAGG
 CCCGGTTGATTGCTCGGCCCTGCCGGATGCCACCCNGCCCTGGTGTGATCCGC
 NGCTTCTGCTGCCTGCGACACCCACNACTGGTGGCACCCGGGAGCTTAGCTGGC
 CNACTCCAGACNTTCCACNAANGTGCNNCCAAATGTNCGNANTGTCCTCGGNTCC
 GNTTCCACNGGTTACGGGCCNTCCGGCTNCCCTCCAACCAAATACGCC

Clone Rv113

:::::::::::Rv113SP6.seq:::::::::::
 ATACTCAAGCTTTATGGTATCGCGCATCACCTGGTTATGAACACTGGAAGCAGCGCAGCGCTTC:::::::::::Rv113T7.seq:::::::::::
 AAAACNGCTTCCATATCCGGACGAAAGAACGCCAGTCCGTACTTAACCCCTCCGGAACCG
 CAGCGCTTCTCCACCAACCGGGCCGGGTGT (SEQ ID NO. 29):::::::::::Rv113T7.seq:::::::::::
 TCGGCTCAGGCCGCGCTGCTGGTAGAGTCGCTGACCGGTGGAGGTTTCGACAATGTGGTGC
 GCCATCGAGACACTGGCGCAGGCTATCGCACCGTTATCGGTACGAAGCAATCGCGTATGC
 GTCGGCAGCGCTCGTATGGTGGAGCAGGGAAAGACCGAGATCGCGTCAAGCATGTGT
 AGGACTGACCTCTGGTGAACGGCATGTTGGTGCATGCGTGGCCGGCGTCTTGGC
 TAGCGAGGTAGCGAATTCTGTGGCAGCTCGAAGGGTCTGGCTGGTGCCTTGGC
 TACGGTGGCGGGGTGCGGCCCTGGCGCGCC (SEQ ID NO. 30)

Clone Rv114

:::::::::::Rv114SP6.seq:::::::::::
 CAAGCTATTAGGTGACACTATAGAATACTCAAGCTTCGCGTCTACGCCGGCCGG
 GGGCCGCAACATCGTTGTTGGAGCGGCCATCCANACCGTTGGCGCCGTAAG
 CTGGTGGCCCGGCAACCGCAAGTCCACCGCCGAGCTGGANGACTACT
 TTGATCAAGGCACCCCTGGTACCGTGGATCGACATTTGCCAACCTGGCG
 CGGGTCAAGGCCGGGCTGCCCTGGTATGCCCGGGCATGATTCTGGTAT
 CCCNNGAAGAACCG (SEQ ID NO. 31):::::::::::Rv114T7.seq:::::::::::
 CGGTTGGCCACCGCTCTGGGCGCTCGACAATGACCGTGTGCTCTG
 GAGCCCCAGCACCTCAAGGCCACCTCGCGCAGCACCATGCCGG
 GCCAGGCTCTCAAGGAAACGCCCTACGGCGTACCGCAAGTAC
 AATCGCGTTGACGACCAAGCGTCGCAACGCTTCGCCCTCAC
 TGCAACCTTCCAGCAATGGCAACAGATCGGAAGCGAN
 CTGATCTGTCTGGTGCN (SEQ ID NO. 32)

Clone Rv115

:::::::::::Rv115SP6.seq:::::::::::
 CCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTTGGCTGG
 GTGCGANAGCGGGCTGGCGCGCACACCCACTGGCCGG
 GGAANATTCCNCTGTTGATGCTGGGATTGCCACGCC
 CCAATCCCCCTCCCTCAACTTCCNAACAAATCATT
 CCTGCCG (SEQ ID NO. 33):::::::::::Rv115T7.seq:::::::::::
 GCGCGCNCAATGCCAATCCCCGAAGACATCATTGGCA
 GCTCGAACATGCGGTGCAACCCATT
 CCAAAATGTCGTCGCCAACCAAGATGCG
 GTCNTCAGCGGCCACATGGGTGCAAT
 ACGGTCCGANGANGCGCAN
 CCTGCCG (SEQ ID NO. 33)

Clone Rv116

:::::::::::Rv116SP6.seq:::::::::::
 ATACTCAAGCTTGGCCAGCCGTCGATGACAAGAAATAT
 CGGTACCGGCCACCGAGTCGATGCC
 AGCATTCCGCAATGCCAGCTGCG
 GCCCCGCCAAATTCCA
 AACAAATGCA
 CCTGCCG (SEQ ID NO. 35)

:::::::Rv116T7.seq:::::::
 CCACCCGTGTATTTGGGATGGGCAAAAGGCGAAGCACCGCGTGGCACGAACGCCGGGAGGGACAATCTCGGGCGG
 CTAGGGCTTCTCGCGGGAGGCCGAAACGTACGGCGTTCAACACGTCGCGTCGCCCTCCGACCGCGAACATTCGGGG
 ATGGCAGCAACCTGGTAGCACCTGGCGGGGATGATCTGCAGCGTCGCCCGGGTAGTCGCCGCCGGCGCTAC
 AGTCTGAAACCGGATGACCATCGATGTGGATGCAGCATCCGACGCAACGGTCTACACGGGATATGTTCGCCTC
 CCTGCCCCGT (SEQ ID NO. 36)

Clone Rv117

:::::::Rv117SP6D2.seq:::::::
 CTGCCCATGTTGGGACGCCGACCAGCGATGCTGGAGGCCTACACGGCCCTTGGTGCCTGGCACGGCACCAGA
 GCGGCTGCAACTGGCGCTGGTAGACGGCAATACCTACCGCAGCCNGACCCNTNCNAANAGGATNTGTTGCC
 GGACCCNCTC (SEQ ID NO. 37)

:::::::Rv117T7D4.seq:::::::
 CCGACTTCCCGGGTACCGCTCAACTTTGTGTCGACCCCTAACGCCATTGCCGGCACCTACTACGTGCACTCCA
 ACTACTCATCCTGACGCCGAAACAAATTGACGCAGCGGTTCCGCTGACCAATAACGGTCGGTCCCACGATGACCCAGTACT
 ACATCATTGCAACGGAGAACCTGCCGCTGCTAGAGCACTGCGATCGGTGCCGATCGTGGGGACCCACTGGCGAAC
 TGGTTCAACCAAACCTGAAGGTGATTGTTAACCTGGCTACCGCAGCCCTT (SEQ ID NO. 38)

Clone Rv118

:::::::Rv118SP6.seq:::::::
 ATACTCAAGCTTGTACACCAAGTGTTCGACCAGGCCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCAGGT
 CGCCACCACGCTGGTCAGTGCCTGCTGAGCTCGTTGCCGCTGCAGCAGCCATTGGGAAATACCTGCCCTGGCG
 CAGCTGGGGATCCAACTTCAATGGTTCGGCACGGGTGTCAAATTACGGTGGCGTAGCCGTTGCCCTAATTGGA
 CCGCTATCGCTGCTTCGGTACCCGCCACAGGCTTCGGCTCAGCCCCATCAGGGCGAACATAACTT
 CAAGAGCACC (SEQ ID NO. 39)

:::::::Rv118T7.seq:::::::
 GAGGCAGCTGCCGGCAATTCTACTAGCGAGAAGTCTGGCCGATACGGATCTGACCGAAGTCGCTGCCGTGCAGCC
 CACCCCTCATTGGCGATGGCGCCGACGATGGCGCTGGACCGATCTTGTGCCGCTTGCCGACGGCAGCGCGTAGGTGG
 TCAAGTCCGGTCTACGTTGGGCTTGCAGGGTCCCAGCCTGGTGCCTGGCGAAAGCGGGGGTCGG
 GTGCCATCAGGAATGCCTACCGCCGCGGACTGCACGGCAGTGCCTGGCGATGTCAGCCATCGGGACATCATGCT
 CGCGTTCAACTCCTCGACCAGTCGGCGAACAGCTCGATTCCGGACCGCCAGCGATTGGTATGGAATCGCGA
 ACTTGGCCACCCGCTGGGTGTTGACATCCTCGACGGTGGGAATTGCCCTCGTAAGCTTGGCGTAGCCTTTTC
 ATC (SEQ ID NO. 40)

Clone Rv119

:::::::Rv119SP6.seq:::::::
 ATACTCAAGCTTCACTGACAAGGGACGAATTCTCGTCGGCCCTGTTGACTGGTGGGCCGAGCTGGTCGCCACCA
 CTCAGGCCGGTACGGCGGTACCCGGCGGGAGCAAACCTGCCGCGGGATGCCAACTTCTGCCGACCATCACCG
 CAGACGCCGGCTTCGGACCCCTGCTGCCACACAGTTGGCAACGCTTAATCACCGCAAGCTTGGGAATCCA
 CGCCCTGTTCGC (SEQ ID NO. 41)

:::::::Rv119T7.seq:::::::

TCCATACCCGATGTGGCNGGACTGCCATGTCATCTAACCTACCCACCTCCGGCGTGGCGTTGCCGCCGG
 GGGTCCGCGGAACCTCGACGAGGGGGTCGGAGAAATGCCANACCCCGCTGAACCGCGACCAACCCGCTGTTGGAGA
 TGTACTTCGTTGAGGGCTTGCCAACCAACCGGATCGCGTGGTTGCCAAAATTACCATGCGTTGGCTGACGGTGTG
 CCTCGCAACATGATGCCACGGGATGGATGCCGCCGGACCGGAGGTGCCCTATGCGCTGACGGTGTG
 CTACCAAGCGGCA (SEQ ID NO. 42)

Clone Rv11

:::::::Rv11SP6.seq:::::::
 AGCTTGCAGTTGCTGAGTAATGTCGGCAACGTCACCAACCGCGATGAATTCAATCATGCCGCCAGGGCGGCCA
 ACCCAATGGTGGCGCGAGCGGCAGCTCGATCGCAGCGCGAGGTGCTGCCGCCAGTTGATTCAACGAAAGGGTGA
 GGTCAAGGCGGGCAGGATAGTGACGAAGGCAAGACCTCATCTGCCGTCGGAAGAAGTATCGAG
 (SEQ ID NO. 43)

:::::::Rv11T7.seq:::::::
 AGCTTCAGAACAGGCCCTGTTGTCGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGCGGCCGCACCG
 CGGCATCTCCCGGTACCGCAGGGCCGCGGCCGACGCCGACGGCGTGTTCGCGCAGTTCGCGTCAATGATGC
 TGACCTGATCGCCACCCGGCGTTCTCGGCGTCGCGTCACTAATCGCGTGTCAAGCAGCGTCTGACAGCCA
 CCACCCGAGTGGCAGCCAGCTGCTCACCGAACCGCAGCGATGCCGTC (SEQ ID NO. 44)

Clone Rv120

:::::::Rv120SP6.seq:::::::
 ATACTCAAGCTTCAGTTCTCCACGACGGCTTCCAAATGAATTTCGGATCCCACAATCTCGGTTCAGATAACAGGTC
 GCCATACCCCTACTTCGCAACGCTGGCGATTGGCCCTGCCGTCACCAAACCATCAAACGCCCTCAAATTGCCG
 GCAATCTCGTTCAGCCAATCCAT (SEQ ID NO. 45)

:::::::Rv120T7.seq:::::::
 GCTCTACGCCGCTACGGTCGAACATGCATCCCGAGCAGATGCTCGAGCGCACCCACTGCCGATGCCGGAAC
 CGGTGGTTACCCGGGTGGCGCTGACGTTCGGCGGAGGACATCNGTGGAAAGGGCGCTTGCCACCGTCGTCNA
 AGACCCAAATTGAGGTGTTGCTGCTGCTACGACATGACCCCGGCGGAGAGAAGAACCTTGACCGGTGGGAAGG
 CTCCGAGTTCGGTATCCACCAAGAAGATCCGATGCCGTTGGAGCGCATTCCTCGGACACCACACGGATCCGTCC
 TCG (SEQ ID NO. 46)

Clone Rv121

:::::::Rv121SP6.seq:::::::
 ATACTCAAGCTGCCAAAGAGACCTCGTCCACCAAGCAGGACGCGACCGTCGAGGTGGCGATCCGGCTTGGCGTCGAC
 CGCGTAAGGCAAACACAGATGGTCGCGGACCGTCAACCTGCCACACCGGACTGGTAAGAAACTGCCCGTCGCG
 GGTTTCGCGGGTGGTGAAGGCCAATGCCCTGCGTTGGCGATGTTGTCGGGAGTGACAATCTGATCA
 AAAGGATTCAAGGGCGGTGGCTGAAATTCAATGCCAATCGCAGACACCGG (SEQ ID NO. 47)

:::::::Rv121T7.seq:::::::
 CCACGGCGTGGATCAAGGTACCGGCCGGATGTTGCGCAATGGCAGGTTGTTGCCGGCTTGATGTCGGCGTTAGCGC
 CGGATTCCACCACATCCCCCTGCGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCCATCGAGATAGGGAGCA
 ACGCAATCCGTCGGTACGGTTCGGGCGTACTCGATGTGCGGACCTGGCGTTGACACCATTTGTCATTGCGGC
 GAAAGTCGATCATCCGTAAGCGCGCTTATGACCGCCGCTTGTGCCGGTGGTAATCCGGCATGCGCGTTGCGTC
 CACCGCAGTCAGCGGGCGCACCAGCAGCTCTCCGGGTTGACCGGGTNATCTC (SEQ ID NO. 48)

Clone Rv122

:::::::Rv122SP6D2.seq:::::::
 GCAGCATGACGGCGGTAGCGAACACCGCCGGATGCGAGCGAAGTAGCGTCGATGTGCTCACGGAATGCCCGGCACC
 GCGATCTCGANGATCACCAAGTGCCACCCCTGCGAGCGCNACACCGACGATTCCGTACACCGCCACGCCGATAGGCC
 TGGCCATCTGATTGGAGCTGGCGTANATGGCGCGATGGTACGATGCCAGCGCACATACATTGTGGCGGCCAGA
 ACCACGGCGTGGGGCGGGCGTCAAGACTAGGCGACCGAGATGCCGGGGTCAACAGGTTGACCATCAGAAAG
 CCTGCGACTAGCACGGCGGCCACTAGGAAGTACAAGAANGTGGCCACCCACCCATGCGGATCGGGTAAGGCTGA
 TGGTCCCGAAATCGACTCCGGCTAATACATGACTCTCCTTGTGCGTACCGCCTTACTTGTGCGCGGAA
 (SEQ ID NO. 49)

Clone Rv

:::::::Rv123SP6D2.seq:::::::
 GGGACACACCTCGATGCTGCCCNATGGACGCGGTGAAACGCAAGCAGCTGATCGAGCTACAACGCCGCGGAAACGC
 TTCCGCCGCGGGCGTGAACGCACTCCGTTGACCGCCGGANCNCTCTCTA (SEQ ID NO. 50)

:::::::Rv123T7D4.seq:::::::

TGGCGCCTTTCGGCTTCCCNNTTAAACGNAGCANGACATTCTGGGTATCGAGTTGACTGGATGGTGTGGG
 ATGTCGGTGATCCTGCTCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCGGTTGAAAGAGGAATTGGG
 GCCGGATTGAACACCGGAAATTATCCGTGCCATGGCTGGTACCGGGGGAGTGGTGACGGCTGCCGCATGGTGTGCG
 GTTACCATGTCGTTGTTGTTGAGCGATTGCGAATTATTGGTCAGATCGGTACCCATGCCCTTCCC
 (SEQ ID NO. 51)

Clone Rv124

:::::::Rv124SP6D2.seq:::::::
 CCGATCGGCCGCANCTGGTGGTNCGGATGAATCCGAGCGAAAATGTAGCTGCGGTGGCGTGTGACTCG
 TNGCGTCGACGCTCGTGGCAGCCACCGANCGGTGGTCAGGATCTGGATGGCAAAGTTGTCAGATCGGTACCCATGCCCTTCCC

ACGGCCGATGAGCTGACCGAGGTCGACAGCGCCGTGTTGGCTGACTTGAACCGACATGGAGTCGCCCGGTTGGCGT
CACCTCAAGCATTCAATGGTTATGCGACCAGTTTTGGGTTACGCCGTACGACATCACGTGGAGACTTGGATGAGC
TGTGTCTGCCAGATAGCCCCAATCGGGACGACCGTGGTACCGTGCGTCTGACCAACTCGGGTCGGGTCGCCGCGCT
ATCGGCATGGGTGCGTNATCACAGCGACACGCCCTGCCAAGGANGTNCGNCGGACC (SEQ ID NO. 52)

:::::::::::Rv124T7D4.seq:::::::::::
CGGGTTGGGATCCACGCGTGCAGGGTGTACGGCACTGAACCGGCCACAGCTGCCGATCCGCTTTCG
TGTTCTCGATCGACTGCCGTAGGCATGCGCAGGCCCTGCTGAATATCGGTACACGTAGGCCGGCTTCCNC
TTA (SEQ ID NO. 53)

Clone Rv126

:::::::::::Rv126SP6.seq:::::::::::
CTTGATTGTGATCATCATGACGATCATCACCTAATTTGCTACCCGACTGGTATCGTGGTACCGTGTGCTTC
CATGGGCGCCTCTTCGGGTTCCGTATTGGTCTGGCAGGACATTCTGGGTATCGATTGTACTGGATGGTGTG
GATGTCGGTGTATCCTGCTCCGGGTGGGATCCGACTAACATCTGCTGCTGATTCCGGTTGAAAAAGGAAATTGG
GGCCGGATTGAAACACCGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTACGGCTGCCGATGGT
(SEQ ID NO. 54)

:::::::::::Rv126T7.seq:::::::::::
GGGGATCCCTAGATCGACCTGCAGGCATGCAAGCTTGGCGTGTGCTTCAACCCGAATTGGCTTCGGGCCATCGGT
GAGGGGGACACACCTCGATGCTGCCCATGGACGCGGTGACGCAAGCAGCTGATCGAGCTACACGCCGCG
AACGCTTCCGCCGCGGGCGTACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATGCCACCG
GAGCNACTGTCAGGCGGGCGTGCAGGTGCCCCGGCGACGGTGCAGACAAGGTGGTGTGCTGGCGTCCCGATCGGC
CAGACGACATCGTGGCGAGATTGNCGGGTACGCCGATGAGGTGGTGTGTTGGCAGGCCGGTNGTCTTCGCC
NCGGGCGANGTTACCGCAACTTACCCAGACCTCCGACGAGGTGGTGGCGTCTCGATCGTC
(SEQ ID NO. 55)

Clone Rv127

:::::::::::Rv127SP6.seq:::::::::::
AAGGCTGCAGGTCGAAGCGGNTGGTTACGACTCCCTGTGTGATGGACCAGTTACTATCTGCGTCTACACGGCC
TTGGTGCCTGGCACGGCAGCGGGCTGCAACTGGGCGTTGGTACCGGCAATACCTACCGCAGCCCCGACC
CTGCTGGCAAAGATNATCACACGCTGACGTGGTTAGCGCCGGTCAACGCGATCTCGGCATTGGAGCCGGGGTT
GAACTGGAACACCGCAGCTCGGTTGAGTCCGGACTTCAACCGGTTCAACCGGCTCGA (SEQ ID NO. 56)

:::::::::::Rv127T7.seq:::::::::::
CTTCCCGGGTACCGCTCAACTTTGTGTCACCCCTAACGCCATTGCCGCACCTACTACGTGCACTCCAACACT
CATCCTGACGCCGAAACAATTGACGCGNGCGGTCCGCTGACCAATAACGGTCCGCTCCACGATGACCCAGTACTACAT
CATTCGACGGAGAACCTGCCGCTGCTACAGCCACTGCGATCGGTGCCGATCGTGGGAACCCACTGGCAACCTGGT
TCAACCAAACATTGAAGGTGATTGTTAACCTGGCTACGGCAGCCGGCTATGGTATTGACCTCGCCGNCATGT
TGCAGACTCCGTTGGGTGTTCCAGANGTCAGGCCGGTGTACGCCGACGCTCGTC (SEQ ID NO. 57)

Clone Rv128

:::::::::::Rv128SP6.seq:::::::::::
CGGTACAGCCCTCGGGTCCGGCCAGCACTCCGCAAGGCTTCGTCGGGGTGGTCGCAGCGCATGGCCACCATCGCA
TTCACCAAGGTCTGCGCAATCACCAGCACGTAGCGTTCTTCTTAAGCAACACCGAAGTTACGACCCGAATGC
TCCGGGAAACATGTACCGTAGGTGGTATTCCGGTACCCGGCTGAGCATTGAGCACGCCGGCAGCACCGCACGAGC
CAGGCAATCAGCCGCCGCCACCGATCGGGTACCGAGCTGAGTCCGGAGACAATGCGGGCGACGCCGGNCTC
CGCGGGCACCGCTACNGCCGGTGG (SEQ ID NO. 58)

:::::::::::Rv128T7.seq:::::::::::
GTGATGGCACGCCACCGCGACACCAACCCGGCTGCGCTACNTCGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCG
CCAGTGTGCGGGCCCTTTGAGGTCGAGGTGCGATACCGATTGCGCATCCGCANCGCNCCCTGGACGACAGAAC
GTGCCCTACGAGTGCTTGTGGGGGGCAAAGAACAGCTGGCATCTGGCGGATTGGCCGGCGGGCTGGTC
GCCAAGGACGACGCCGTTCCGGTGTGATCGACGAGCGCTGGGGTTACCGATCCGGAGCGACTATCAAGATGGGG
AGGTCTCTGACACCACGCCCNACGGACATGTGATCGTGCACGTGAGTCCCAACCCG (SEQ ID NO. 59)

Clone Rv129

:::::::::::Rv129SP6.seq:::::::::::
GCGAAAGTCCGTTGGGTGCAATGATGATGAGTAGCGCTTCTCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGT
TCGGGTCGACTCGATGTGCGCAGCTGGCGTTGACACCACCTTTGTCATTGCGGGCAAAGTCGATCATCCGGTNNG

CGCGCTTATGACC CGCCCTTGTGCCGGTGGTAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGAGCGGGC
GCACCA CGCGACTTCTCGCGGGTGTACCGGGTGTACCTCGCGAAATCAGATA CGCTGGCGCGACGACCAGGCGTC
TGGGCTTGTNCCTGCGAATTGNCATGTCTAATCANGTCTCTCACGCTCTCGTCGCCGGCTAGGCCGATTGCC
CTGCTCCTCCTCATCGCTTCGCTCTGCATCGTCCCCGGCTAACGCCGTGCCCG (SEQ ID NO. 60)

:::::::Rv129T7.seq:::::::
GATGGTTCGCGCACGGTCAACCTGCCACACGGACTGGTAAGACTGCCCGTCCGGTATTGCCGGTGGTAAAA
GGCCGATGCTGCCGTTGCCCGGGGGATGTTGTCGGGAGTGACGATCTGATCGAGAGGATTCAGGGCGCTGGCT
GGAATTGATGCCCGATCGCAACACGGATCAGAATGGCAAAGTCCGTCGCATCGCTCGGGTGTGGTCCGCGC
GGCGTGTGCCAACCGAAAACCGGACCGTACCCGACTCCCCATGGCGTCCCGATATCAAGGGCCGGCAAAT
CAACTTCCC GTGATCAGCAAGGCAACCTGCCCTCCCG (SEQ ID NO. 61)

Clone Rv130

:::::::Rv130SP6.seq:::::::
ATACTCAAGCTCGTCATAAGACCATGGTGCCTTCTTCACCCGTCCAGAGTCGGGGCATCCGACCCGCTCGCA
TCGCATCATCCTCCCACGACGGCGCTCATCAGCTTGGCCATTCAATGTA CTTGATACCCCGCTGCGGGTAGG
CCACTGCGACAATTCAAACACGGTGTACACGGTGAATAGTGTGAGATGGGCTCTGATCAACCGTCGAAACCGGT
TTCGCATCAATAGCGGAATCCCACCGGGTTGCATGGAGGCTGCTGACCTTGGAAAACAAAATTTTCAACACAA
AACAAACGCCNCGGAAACTTGCA (SEQ ID NO. 62)

:::::::Rv130T7.seq:::::::
CGAATT CGCGTGCACCGCTATGGGTGCGAGCAGCGGCTGGCGCCGACACCCACTGGCCCGGGTGTTCGCCCG
AACCCGGATCATGGT GAGCGAAAAGGAGATT CGCCTGTTGATGCTGGGATTCGCCACCGCGAGGCCATCGACCGATT
ACTCGCACCGGGTGCAGAGGGTGCAGTCCGCTCCGTCACGCTCTCCGACGATCCATCGGCTTCCGCGTC
GGTGGCGGTAGCGTGTGAAATCGTGC CGCCGCTACCTGCAAGGTGATTCTGTCGGTGTGCGAAGTGCCTT
TCGCATCGACTTCCGTTGACCTACCGCTGGCGTCCGACAACACCCCGGTGAGGCTGTTTGTGCGAGTTGG
GCGGAATCGTGTCTGGTTACAGCCCCGACTCGTACGGCGTGC CGCCGACGGAGTTGTTATCACCGATCCGT
TGGCGTACCGCGCTTGGC (SEQ ID NO. 63)

Clone Rv132

:::::::Rv132SP6.seq:::::::
TCAGACTCCACCCAGCAGCAGCGAGCGAAGCTGAATCTCAACCGGGTTGTCGATCCGACAGGTTGGGTGCG
TTTGGGCAATGACAGGTGGCGCGGTGCGTTCGGTCCGGCGAGGTGCTGCGTTGGGATCGCCCGGCTGGCA
TTCNGCGTGTGGCGCGCCGGTGGGGGGCAACAGGTGTCGCCGTGCGGGTGGCGTCAGCGGTGACGGC
GGCGAAGCGGCCGTTGTGGGTACCGGGGGCGTGGCTCCGATCGCGTTGGCGTGC CGGCACCGCAACGGTCA
AAGCTGGCGTGGC ATCGCGCAGTACGCCAGTGCCGCAATCGTCCCTGCGACGTGCAAGTNGGGTCCACCTGA
TGCATGGCAAAGAACCTACCGTGTAA CGCNAACNCAAGGACCGCGCCGGTCG (SEQ ID NO. 64)

:::::::Rv132T7.seq:::::::
TTTCCCGGGTACCCGCTCAACTTGTGTCNACCCCTCAACGCCATTGCCGACCTACTACGTNCACTCAA
CTACTTCGACGCCGAACAAATTGACCGCAGCGGGTCCGCTGAACAATT CGGTCCGCCCCAGAAAGAAC
AGCTTTNCNTCTTCNCACGGAGAACCTGCCGCTGCTAGAGCCACTCGGATCGGTGCCATCGTGGGG
AACCCTGGCGAACCTGTGCAAGGCTCTAGTTTCCACCTCCGCCCCNTCTCGCCCC
NTGTTTCAATACTCCGTTGGGTGCCCCAAA (SEQ ID NO. 65)

Clone Rv134

:::::::Rv134SP6.seq:::::::
GCTTCCGGCTCGTATGTTGTGGAATTGTGACCGGATACCAATTCAACAGGAAACAGCTATGACCATGATTACGC
CAAGCTAGTTAGGTGACACTATACAATACTCAAGCTTGCCTGGCGCCGACCACTTCGATGGCACGACCCGTGA
ACTGCTGCCCGCCAATTCTCTGCGCCGACCGATGGGACCGCGCTGGGATTCAGAAGGTGCCGATCCCGC
CCCTGGAAAACCGCGTGCACCTACTTCACGACCAACGAC (SEQ ID NO. 66)

:::::::Rv134T7.seq:::::::
CCGATCGACTGATGCGCCGACAACCA CGCCCCAACACTGGAAATGAACCGTGTGACCATCATCAGCACCGGTTGTA
GGCGACTT GCGACATGTTCAACCGCCGTACTCGGACGGATCTCAACCGAAACAGCCAGCTCGGCCAGGCC
CACGTA CTGTCGGGGATCTGGGACCCAGCTCGAGGACGCTGCCGTACGGTGTCTAGGAATTCCCGCAGTTGAC
CAGAAACGCTCGGTTGGGCTCCTCGCGTCCGACGGCTGGGAAATGGGTGTATGAGCCCTACGGGAAACCGGCC
CACAAAGAGTTCTTGGCGAAGGACGGTTATCCAACCACCTTCGCGAGATTCCCTCGGCAAGGGCCCGCTTGCTC
CTCGGTGACCTGAGTTGCTGTGCCATCGCGCCTCCCTGA (SEQ ID NO. 67)

Clone Rv135

:::::::Rv135SP6.seq:::::::
 TGCACTCCGGCTCGTATGTTGTGGAATTGTGAGCGATAACAATTACACAGGAAACAGCTATGACCATGATTACG
 CCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTACGGTATCGCGCATCACCTGGTCATGAACGGAAAGC
 AGCGCAGCGCTTCTTCCGGCCGAAACATGAGCCAGCCTCTCGTCGGCGGTGAGGTGCTCGGGCAGCTCGG
 CCGCGACAGCGCCTGACCCCTGAAACCAAGCTTCCATATCCCGCAGAACGACGCCAGTCCGCTACGTAACCCCTCCG
 CGACTGTCCATGGACAAACAGCGCTCTCCACCGACCAGGGCCGGGTGTTGGGTGTTTCGGCGACCGCAGCCAGGTG
 GTCCACACTGCCGACGGCGCCGAGCCGTTACCGACCAGGCCGAGCAAGTCCGCCGATCGCATACTCC

(SEQ ID NO. 68)

:::::::Rv135T7.seq:::::::

GGGGCGCTGCTGGTATAGTCGTGACCGGTGAGGTTGACAATGTGGTGCCTGGCGCTACGTGCCATCGA
 GACACTGGCGCAGGCTATCGCACCGTTATCGCTACGAGCAAATCGGGTATCGTTCTGAGCATGAGTCGGCAGC
 CGTCGTATGGTCGACACCCACGACGGAAAGACGAGTCGGCTCAAGCATGTGCGCGGATTATCAGGACTGAC
 CTCCCTGGCTGACCGGATGTTGGTCGCGATGCCCTGGCGCCGGCGTGGTCGTTGCGATAGCGAGGT
 CAGCGAATTCTCGTGGCAGCTGAAAGGTCTGCCGGTCTTGCACACGATGGCGAGGTTACGGTCG
 GCGGGGTGCGGCCTGGCGCGCCAGAGCACGAGTCACCGATGCGCAGCTAGTGGCGACAGCGTCAGCCAAC

(SEQ ID NO. 69)

Clone Rv136

:::::::Rv136SP6.seq:::::::
 TGCTTCCGGCTCGTATGTTGTGGAATTGTGAGCGATAACAATTACACAGGAAACAGCTATGACCATGATTACG
 CCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTCCGTACAGGTGCGCTCAAACACGGGGGAAAGCAGACACCA
 GCCTACCGAGCTGGAGTCCAGGACGCCAGCGCGCTCGGTCTGCGTGGTGCCTGGCGCCGGGGTGGCGTTGGCTGG
 CAACGATCTCCACCCAGCCGGTGGTTACCCACGATCTCGCATAGACGCGGGCGAGGCCGGTGCATACCGTATT
 GCGTCAATTGGGACGCGGTTGTGCATTCTGGTAGCTCGTTGCCACACCGTCAGGGGTTGACGTTGGCGGGTTCGG
 CGGGCCCGACCGCTGTCACCATGCCGCAAGCCGACCTGCGGCCACCAACT

(SEQ ID NO. 70)

:::::::Rv136T7.seq:::::::

CGGCATGACCACCGACAGGCCGACTGGTCGTACCACTCGAACGCCGGGTGTTGATGTCCAGCCGCTGAAGTCGT
 CTGCGCGCGCAGGCCGTCGAGCAGGTACAGGGCGAGTTGGCACCACCTTGGAAATTGGACCTTGTATGTCAGC
 GCCCATCGACGGCGACGCCGACCTCGCAGGTACTCCACCGCAAGCCGCCGGAAATGCCCGCGGTGCGCGTGC
 ACCGACGCCGACCCGACACTAGGGCCGCGCACGCCGACCGAGTCGACGCGACATACCGTGAC
 GGCGCCACGAAACCTGTCACAAAGCTGCATTCTGCTTCCCTCATCTCATCTCAACGACATCCATGCATGTTGGCG
 CATCTGAATTANGTCAGACTGCAGGCCTGGCGCGAGTGCTGTATCAACACAAACTCGGGCGT

(SEQ ID NO. 71)

Clone Rv137

:::::::Rv137SP6.seq:::::::
 TTCCAACCTAATTGGCTTCTGGCCCATCCGTGAGGACGGGTGCTCAACAACACGTCGTCCCGGGACA
 CACCTCTATGCTGCCATGGACCGGTCAAACGCAAGCAGCTGATCGAGCTACAACCCCGCGCGAACGCTTCCGC
 CGCGGGCGTGACCGCATCCGTTGACCGGGCGATCGCGTGTATGCGATGACGGCATCGCCACCGGAGCGACGGCC
 AAGGCGCGTGCCACGTCGCCGGCGCACGGTGCAGGACAAGGTGGTGTGGCGGTCCGATGGCCCAAACGACATC
 GTGGCGAGATTGCGGGTACGCCGATGAGGGGGTGTCTGGGACGCCGGGTGTTCTTCCCGCTGGCGAGGGT
 TACCGCAACTTCAC

(SEQ ID NO. 72)

:::::::Rv137T7.seq:::::::

CAGGCATGCAAGCTTCCGCCGATACCCGCATGTCGCCACATCCAGGACTTCTGGGGGATCCGCTGACAGCGGG
 GGATCCAAAGTGCAGTGTATGGCCGCTACGTCGTGGTGTACCTCGTGTAAACACGAAACCGAAGCGTATGAC
 TCGGTCCACCGGGTGCAGCAGTGGGACACCACCGCCACCGCACGGGGTGAAGGCCGATGTCACCGGTCCGGCA
 GCACTCAATGCCGACCCAGGCCGAGGCCGGAGACAAAAGTATCGTAAGGTACCCGATCACNAGCATGGTGTGATCG
 AGCAATGTTGCTAGTGTATCGCTCCGTAATTACCGGGTCTCGTCTGATCATGGTGGCATCGACTCGGCCA
 TCCCGGATTATCGCCTGCTGCCGAAACACAACTTACCTTACACATTGCAACACTGCTCTCAT

(SEQ ID NO. 73)

Clone Rv138

:::::::Rv138SP6.seq:::::::
 CACTACTCAAGCTCTCTCNCTCATTACCAACCCCTGTAATTGGGATGGCAAAAGGCGAAGCACCGCTGGCCACNAA
 CGCCGGGAGGGACAATCTCGGGCGCTATGGCTTCTCCGGGAAGGCCCAACGTAACGGCTTCAACACGTCGCGTC
 GCCCTCCGACCGCGAACATTCCGGGATTGGCACCAACCTGNTACCACCCCTGGCGGGCGATGATCTGAGCGTCGCC
 CGGGTAGTCCCGCCGGCGCTACAGTCTGAAACCCGATGACCATCGATGTTGGATGAGCATCCGACGCAAC
 GTTCCTACACGGCGGATATGTTCTCTCGCTGCCGAGCCGGTGGGTCTATCCCGTGAACACCGACATCCN

(SEQ ID NO. 74)

:::::::Rv138T7.seq:::::::
 CAGGCATGCAAGCTTCGTCAGTTCATTCGCGCAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGG
 CCAACGGTGATTCTTGGCCGCGCTGACGGCGAAGCAGACGCCAGCGACCACATTCAAGCAGATGGCCAGCGCGTGCC
 GGGCCACGAGGTTGGTGTGCGCGGTACTCCCAGGGTGGCCGCGTGTATCGACATCGTACCGCCGACCAACTGCCCG
 GCCTCGGGTTACGCAGCCGTTGCCGCCGAGCGGAGCATCACATGCCCGATGCCCTGTTGGAAATCCCTCGG
 GCGCGCTGGGGCTGATGAGCGCCCTGACCCCTCAATTGGGTCCAAGAACATCAACCTCTGCAACAACGGCGACC
 CATTGTTGGACGGCAACCGGTGGCAACGCACCTAACGCTACTTGCCCCGGATGA (SEQ ID NO. 75)

Clone Rv139

:::::::Rv139SP6.seq:::::::
 GTTATGCACTGGTTAGGTGTTCCATGAGTTTCAATTCTGAACATCCTTAATCATTGCTTGGTTTTTATTAAA
 TCTGCAATTACTGCAAAGCAACAACAAAATCGCAAAGTCATCAAAACCGCAAAGTTGTTAAAATAAGAGCAAC
 ACGTACAACAGGAGATAAGAAGAGCACATACCTCAGTCAGTCACTTATTACTAGCGCCCGCCGAGCCGTGTAACCGAG
 CATAAGCGAGCGAACTGGGAGGAAGCAAAGAAGAACTGTTCTGTCAGATAGCTCTACGCTAGCGCAAGAACGAAATA
 TCCACCGTGGGGAAAAACTCCAGGTAGAGGTAC (SEQ ID NO. 76)

Clone Rv13

:::::::Rv13SP6.seq:::::::
 ATACTCAAGCTGGGTGTAGCCGATACCGGAAGTCNCATGATCAGCCACGTTCCGGCCGCCGGCATACGGTGGTG
 TACCGATCTCCCGTCAACACCCGCGGTAATGCCGACGGTGCCGGTGCAGCCGAA (SEQ ID NO. 77)

:::::::Rv13T7.seq:::::::

AGCTTATCGAAAGCGAACAGCTCGGGCGCCACGACGTGCTGCGTCGGATTGCCGGCGGAGATCAATTCCA
 GGCAGCTCCGGACAATCGGGCTCTGCTGGCCCGAACGAGGACTCGAGGTCAACCCGGTGCCGGGTGTTGTC
 ACCTGCCGATCGCACAGGTTGGCCACAACCGGGCGCTTGATGCCGGTCCGAAGCCCCGGCAGTTGCCAAACCCATC
 GTGATCAGGCTGGCTCGCGAGTCCGGGAAGAAATGGTTGCCCTGATCACCTACCGCCA (SEQ ID NO. 78)

Clone Rv140

:::::::Rv140SP6.seq:::::::
 TCAACACGCCAGCCACCACGCGGGTCGGCGCCGGCCGGCCCTCCAGGCTNCTCCGCTCGGTGATGGCACG
 CCACCGCGACACCACCCGGCTCGCCTACGTCAGCCATACCGGGCGGAGCTACATCGCCCGCCGCCCAGTGTTCGG
 GCCCTCTGCCAGGTCGAGGTGACACCGATTGCGCATCCGACGCCACCCCTGCGACGACAGAACCGGGCCCTA
 CCCACTGCTTGTGGCGGGGCCAAAGAACAGCTTGNATCCTGCCACAATTGCCGGGCCG (SEQ ID NO. 79)

:::::::Rv140T7.seq:::::::

CAGGCATGCAAGCTCAGTCCGTACGGCTCGGGTACGCTCGGTGCGAGTGTATAGATGACGACCGGGAC
 CTCGTCGGCATCTTCCATAGCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGTAGAAGGTCGGCAGCGCTC
 GGCATTGGTCATGGGATATGCCGCTCGGGACGGTCAGAGCCCTGGGTCCGGCAGCACTCCGAGGCTCGTC
 GTGGTCGGCACGCGCATGGGCCACCATCGCATTCAACCAGGTCTGCGCGAATCACCAGCACGTAGACGGTTCTTCT
 AAGAACAC (SEQ ID NO. 80)

Clone Rv141

:::::::Rv141SP6.seq:::::::
 AATATTCAAGCTTCGGCGAACGACNCCTTGCACATTGATAACAAAATAGAAATCATTGATGGTTGAGTCAC
 CAGGCCGATCAAGCCTCGCCGAGCCAATTCAATCAAGAGGCCAACGCCGTACCAATCAGCCCGCAACGAGGGGA
 TTCCGTCNTTATCAGCCNAATAACTGCTCTGGGTACCAACCGAACAGCGCAATATGGGAAACGGTCGCCGTTG
 CACAACTAAATGTCTCGGTATTGTTGATTAAGAACGACCAACCCACCAAGGGCAATCCAACGTAGAGAGCGTTAAATT
 GACCGTAAAACCTCCCGTACCTGTT (SEQ ID NO. 81)

:::::::Rv141T7.seq:::::::

CAGGCATGCAAGCTGCTGCATCTTCCGTGACTGCTCCGAAACCTGGGGTGTGCCTGCTGTATGCACGGCATA
 CGGACATCTCCCTGATACCCGCGGTGACCCAGCCACGTGTCATCATCAGGGGTCAACCCGGCCAAGGGCGAC
 GGCACGCCAACGTTGCCGACCGTTAACCTAGTGTGTTAGCTCATTGCTGCGAGCAAACAGCTGGTCGCCGTTA
 GGAACGAAATTGAAACTCAACCGATTGGTGCCTGCCGCGTAAGGTGTCCTGTCGCCGGTGCCTGGTGTGTTG
 GGTAACGACGACAATGTGACCGGGGAGGTGCAACCAACTGCCAGGGCGTCCGCGAAAGTCCATTGCNGGGGAAAGAAG
 ACAC (SEQ ID NO. 82)

Clone Rv142

:::::::::::Rv142IS1081.seq:::::::::::

GAAAGTCCCCAAGGTGTTGGTAAACTCGCTGGACGGTCCCAGGATGTTGGCAGCACATTACCGGACATGACCGG
 AGCAAGACCGACATCCTCCCACCGTCGCGCGTGTACATCCGTAGCCGCTCTGGCAGGTGCTGGTTGAACAA
 AACAGCCCAACACCTGCCACGACGAAGAAGCGGGTTGCGCATGTCCTGTCGGCTCGGGATCGAATTCTACGA
 ATTCTTATCTACGGGACCGCTGCGCGCTGGTGTTCACCCACCGTGTCTTCCCACACTGGATCCCACGGTGGCCGC
 CGTGGCCTCCAAGGGACATTGCTGCGTCTATCCCGGCGTCCGGCGGCCGTCTTGGATACTTGGAGA
 CCGCCTCGGCCAGAACGACCTGTCGCCACACTGTTGATCATGGGCCTGGCAACCGTGAACGTTGGCTGGTCC
 ACGACAGTGGCCATCGCGC (SEQ ID NO. 83)

:::::::::::Rv142SP6.seq:::::::::::

ATATTCAAGCTTGTACACCAAGTGTCCGACCAANCCTCCATCCGGCAGTGGATACTCCAGCAGGTAGCAGGT
 CGCCACCACGCTGGTCAGTCGCGCTTCATCTCGCTTGCAGCAGCAGCCAGTCCGGAAATAGCTGCCCTGGCG
 CAGCTTGGGATCGCGACGTCGATGGTGGCGACGGGTGCGAAATCACGGTGGCGTAGCCGTTGCCTGATTGGA
 CCGCTATCGCTGCGTTCGGTAGCCNCCCCCACAGGGCGTCCGGTCAAGCCCATCCAAGGCGCGATGAACG
 TCGAGAGCAGCCCGCGCAGCAAATCCGGCTCGCTGTGCGAGTTGGTCAGCCAGAAGCTGCTCGGTGTCATAAGATG
 AGAAGAGGTCACTGCGTCTTCCTTC (SEQ ID NO. 84)

:::::::::::Rv142T7.seq:::::::::::

CAGGCATGCAAGCTTTGAGCGTCTCGCGGGCAGCTTCGCCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACG
 GATCTGACCGAAGTCGCTCGGGTGCGACCCACCCCTCATTGGCAGTGGCGCGACGATGGCGCTGGACCATCTGTG
 CCGCTTGCACGGCGACGGTAGGTGGTCAAGTCCGGTCTACGCTTGGGCTTGCAGCCCATCCAAGGCGCGATGAACG
 GCGTTGCGCCGCAAAGGGCGGGTGGGTGCATGAATGCCTACCGCCGCCACTGCACGGCAGTGGCC
 GGCATGTCAGCCATCGGACATCATGCTCGCTCATCTCCGACAGTCCCGGAACAGCTCCATTCCGGACC
 GCCAACGC (SEQ ID NO. 85)

Clone Rv143

:::::::::::Rv143SP6.seq:::::::::::

ATACTCAAGCTTGGCTGGTCGCCCTCCAATTCAAGCGTGCACCGCTATGGTTGCAGCAGCGGCTGGCNCCGCACA
 CCCACTGGCCGGGTGTTTCGCCCGAACCGGATCATGGTGAGCGAAAAGGAGATTNCCTGTTCGATGCTGGGA
 TTGCGCACCGCGAGGCCATCGACCGATTACTCGCCACCGGGGTGCGAGAGGTGCGCAGTCCCGCTCGTCACGTCT
 CCGACGATCCATCCGGCTCCGCCGCGGGTGGCGTAGCCGTGCGATGAAATCGCTGCCGGCGTACCAAGGTGA
 TTCTGCCCCGTGTCAGTGCCTTCGCGATCGACTTCCGTTGACCTACCGGCTGGGGCGTCGGACAACACCC
 CGGTGAGGTGCTTTGTGCAAGTGGCGGAATCCGTGCTCTGGGTACAGCCCCGAACCTGTCACGGCGGTGCGCC
 GCCGAC (SEQ ID NO. 86)

:::::::::::Rv143T7.seq:::::::::::

CAGGCATGCAAGCTCAACCTATTGACGCATTGCGAAGTGCAGGGCCCGGCATGGCAATCCGGAAGACCATCA
 TTGGCCAGTGGCCGGCGCTAACAGGTTCCAGCCCCCACCAGTGCCTCGAACATGCGGTGCAACCCATTGCGAGG
 CGGCAGGGAAAGCACCGCGAACGCCAACGGCTGCAGTTCCGCCAACATAGTGTGTCGCCGCAACCGATGCGCT
 CGAAAACGCCGCCGGCAGTCAGCGACCCGACCGCAGGTCGAGAGACGTCGTCAGCGGCCACATGGGGTGCAC
 CGGCACGGCAGGTAGGCCGCCAACCCAACCGTGGTCATGCCACGGTCCGAGGAGGGCACCCACCC
 (SEQ ID NO. 87)

Clone Rv144

:::::::::::Rv144SP6.seq:::::::::::

ATACTCAAGCTTCCCGCCGAGGTGACGGCGGGCTAGGCCACTTGTATGCCACCCGATCGACGGNCCTGGTC
 GGGGTTGACTGGCGCCGGCGAGCAGGGCTCAACCGCGCCGGACGTCGGCGCCGTACCGGTGGCCATTGCC
 CGGGCGGGAGTCGTCAGCTGACCAAGGTAGACAGTCGGCGCTGGCGTCGAAGACAAACGTGTCGGGTGTCAGGC
 CGCGGAGAGGCNCGGCGACGTCTGGGTTCTCGTAGAGATACTGGGAACGTCAGCCGTGGCGGGCGCTCGGC
 GACCATCTGATCGGGCCCGCTCGGGTAGGTGACCACTGCTTACTGGAGATAACCGACCATCGGGACCCATTGATC
 GGGGAGGTCCCGCCGACCGTGGCAATCGGCCGGACGTGTCGCCGTACCGGCCAGTGGTTC (SEQ ID NO. 88)

:::::::::::Rv144T7.seq:::::::::::

CAGGCATGCAAGCTTANCACATCAACCCCGCCCGCACAGCACCGACACGATGTCGATGCCATGAGGTGAATGT
 CGAACTGGCNAAACCATCTGGCGACCGCGACCCACGGCAACATGGTACCGCGGATTCGGTGCACGCC
 GACGGGCCGCTCTCACCGCAGGTGACCTCGATACCGAGACCGAGCCGGCGTTACTCACGCACCCCTACCGTGTCA
 CGCCCAAAACGGCGCTGGTGGTCATTGCCGGAGTGCACCCCGCACCCAGTGTGTCGCCGGATCGGCCGACCAATCC
 CGCACCCACGTGCCAAACCCGAAATCACCGTGTGACCGTGGTAACGACCGACAGTAACGTCACTACGGCGCC
 ACGCGACGCCGAACCAACCGCACATGATGATCGCGT (SEQ ID NO. 89)

Clone Rv145

:::::::Rv145SP6.seq:::::::
 ATATTCAACCTTGCACACATTGACGATACTTGGTACAGAGACCCAAAAGCTGGCTCCACCGCGCAGGGGACCA
 CGGTCAACCTTGANNCNGCTTCGATCGTTGATGCTGCGTCTTGGTCCGGAAACCGCAGGCTGGCATATGCACGT
 GGGCGACTGGCAGTCGCGATCCCCACCGATTGCGCCGAATACAGCTTCAGCGCTCCCCAAGTTGATCATCGACC
 GGCTGCCGGATATCCCGCACTTGCAGTGGCGGTACCGGGCAGCCGCTGGACTGGACCAGGGTGGTTCGTCGAGG
 ACCACGAAC (SEQ ID NO. 90)

:::::::Rv145T7.seq:::::::
 CAGGCATGCAAGCTTCATGCCCGCGCATGATAGCCACATGCACGCAATCGAACTCAGCGAAACCGGGCAGGCCAGGCG
 TCTTACGCCACCTCACCAAGCGCGAACCTCAACCCGGCACCGAGACCTCCTGATC (SEQ ID NO. 91)

Clone Rv146

:::::::Rv146SP6.seq:::::::
 ATACTCAAGCTTGTATTTGATCATCATGATGATCATCACCCGAATTGTGGTAGCCGAGTGGTTATCGTGGGTACCGT
 CGTCTTCCATGGGCGCTCTTCGGGCTTCCGTTATTGGTCTGGCAGGACATTCTGGTATCGAGTTGACTGGAT
 GGTGTTGGCGATGTCGGTATCCTGCTNTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCGGTTGAAAGA
 GGAAATTGGGCCGGATTGAACACCGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTACGGCTGCCGGCAT
 GGTGTTGCCGTTACCATGTCGTTGTTGTCTCAGCGATTGCGAATTGGTACATCGGTACCCACCATCGGCC
 GGGCTTGCTGTTGACACCCCTCGTCGTCGCTCGTACGAAACCGTCCATTGCTGCCCTGCTGGGACCTGGTTCTGGT
 GGCGCTACGGTGCAGCCGCCCCAGTCAAATCTTCCGCG (SEQ ID NO. 92)

:::::::Rv146T7.seq:::::::
 CAGGCATGCAAGCTTGGCGTCCACCCGAATTGGCTTCGGGCCATCGTGAGGACGGCGTGGGGTGTCTC
 AACGACGACGTCGTCGCCGGACACACCTCGATGCTGCCCATGGACGGCTGAAACGCAACGAGCTGATCGAGCTA
 CAACGCCGCCGGAACGCTTCCGCCGGCGTGACCGCATCCGTTGACCGGGGATCGCGTGATCGTCACTGAC
 GGCATGCCACCGGAGCGACGGCAAGCGCGTGCCAGGTGCCCCGGCGCACGGTGCACGGGACAACGTTGCTGGCG
 GTCCCCATCGGCCAGACGACATCGTGGCGAGA (SEQ ID NO. 93)

Clone Rv147

:::::::Rv147SP6.seq:::::::
 ATACTCAAGCTTTACGGTATCGGCATCACCTGGTATGAACTGGAAGCAGCGCAGCGCTCCCTTTGGCCGCA
 ACATGAGCCAGCCTCTGTCGGCGGTGGGTGCAAGGTGCTGGGAGCTCGGCCGACAGCCGCTGACCTGAAAC
 CAGCTCCATATCCCGCACGAAACGACGCCAGTCCGCTACGTAACCCCTCCCGACTGTCATGGACAACAGCGCGTT
 CTCCACCGACCAGGGCCGGGTGTGGGGTGTTCGGCGACCGGCAGCCANGTGGTCCACACTGCCGAAG (SEQ ID NO. 94)

:::::::Rv147T7.seq:::::::
 TAGTCGCTGACCGGTGCAAGGTTTCGACNATGTGGTGCCGGTTCGGCGGCTACGTGCCATCGAGACACTGGCGAGGCT
 ATCGCACCGTTATCGGCTACGAGCAAATCGGGTATGCGTTCTGAGCATGAGTCGGCAGCGTGTATGGTCGAC
 ACCACGACGGAAAGACGCGAGATGCCGTCTANCNTGTGCGCGGATTATCAGGACTGACCTCCTGGCTGACCGGG
 ATGTTGGTCGCGATGCCCTGGCGCCGGCGTGGTGTGGCTGGCG (SEQ ID NO. 95)

Clone Rv148

:::::::Rv148SP6.seq:::::::
 ATACTCAAGCTTCCGCCATACCCGCATGCGCACATCCAGAACTTCTGGGGGATCCGCTGACAGGGCGGGA
 TCCAAAGTGGGATGATCGGCCGCTACGTGTTGTAACACAGAAACCGAAGCGTATGACTCG
 GTCCACGCGGTGCGGCACATGGGACACCACACCGCCACCGCACGGGTGAAGGGCTATGTCACCGGTCCGGCAGCA
 CTCAATGCCGACCAGGCCAGGCCAGAGACAAAAGTATCGTAAGGTACCGCGATCAGGACATGGTATCGCAGCA
 ATGTTGCTAGTGATCTATGCCCGTAATTACCGCGGTTCTCGTCTGATCATGGTGGCATCGACCTCGCGCAATC
 CGCGGATTCTGCCCTGCTGCCGACCACAAACATTTCAGCCTTCAACATTGCGACAACCTGCTCGTCTCATGG
 CGATTGCNGCGAAC (SEQ ID NO. 96)

:::::::Rv148T7.seq:::::::
 CAGGCATGCAAGCTTGGCGTGCCTCAACCCGAATTGGCTTCGGGCCATCGTGAGGACGGCGTGGGGTGTCTC
 AACGACGACGTCGTCGCCGCTGGACACACCTCGATGCTGCCCATGGACGCCGTAACGCAAGCAGCTGATCGAGCTA
 CAACGCCGCCGGAACGCTTCCGCCGGCGTGGCAGCGATCCGTTGACCGGGGAGTCGCGGTGATCGTCACTGAC
 GGCATGCCACCGGAGCGACGGCAAGCGCGTGCCAGGTGCCCCGGCGCACGGTGCACGGGACAAGGTGGTGTGGCG
 GTCCCGATGCCAGACGACATCGTGGCAGATTGCGCCGGTACGCCGATGAAGTGGTGTGGCGACCCGGCG
 TTGTT (SEQ ID NO. 97)

Clone Rv149

:::::::Rv149SP6.seq:::::::
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 GAAACACGCGGAGCACCAAATTCACCGCAGCGCCGGGGCGGTTCAACTCACCCTGGATCGCTCTCGTCGTCTGGTGC
 TGGACAATCGCTGAGCGCTCGGAACACCTCAGCTCTGCTGCCGGCTTCTCCGGCATGGTAACCCCA
 GGTTCGCCAACGGTCTACGTAGCGACTGCGACGCCGGTGTCACTCGCATCGACCTGTTGACTCATCCTGTCAGGAT
 GAAGGCCTACTGGGCCACTGCGCTCTGCCGCCAGGTCGGCAATCACCAAGGATCTCAGAAACGAGCTGCGACTC
 ACTCTCCAGGCCACCCCTGCCGAAAGCTCGACATGGTCAATCCGGCCG (SEQ ID NO. 98)

:::::::Rv149T7.seq:::::::
 CAGGCATGCAAGCTTGGGCCGGAGTGGTTCGACGCCGCTCGCTCTCGGCATCGGTTGGCTGTACCCAGCAG
 TTGGTAGTTCTTCAGTACTGTTGTCAGCGTCAGCCGCGCTGTGGTCCGCGAACCGCTTATCTCAATCGAGACGATGCCAGCT
 GCCGGTCAGGGTGCCCTCCAGTCCACGCCGCTGTGGTCCGCGAACCGCTTATCTCAATCGAGACGATGCCAGCT
 CATCGTGTGGCGATCTGTCCGAGGGCACCTCGAACCGCCGCTGCGAGTACAGCCACGCGATCGTGTGCCCTTCGC
 GTCGACCATCGTCGATACCGCAGGCACTGCCCTC (SEQ ID NO. 99)

Clone Rv14

:::::::Rv14SP6.seq:::::::
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 GGCAGCGAAATCAATTCCAGGCAGCTCCCGAACATCGGGCTCTGCTGGCCCGAACGAAGGACTCGAGGGTACCCCG
 GTGCCCGGGGTCGTGGTGCACCTGCCGATCGCACAGGTTGGCCACAACCGGGCGCTTGATGCCCGGTCCGCAAGCCC
 GGCAGTTGCCAAACCCAGCGTGTACAGGCTCGCTCGCAGATTGGCGAACAGGACTGGCTCGCCTGATCACCTACCATC
 GGCCAGGATCTGCGTGTACACACGCTCGCCAAGGAGGGTGTGTTGCTATCGACGGCCTTAGCCAGATGTT
 GGAATCGACTATCGATAGTGTCCCGCCATGGACTTGATCGCG (SEQ ID NO. 100)

:::::::Rv14T7.seq:::::::
 AGCTTCGGTGTAGCCGATCACCGGAAGCCGATGATCACGCCACGTTCGCGCCGCCGGCATACGGCGGCGTACCGAT
 CTCCCGCTCATACACCCCGGGTAATCGCCGACGGTGGCGGTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAG
 TTCCAGGTCCAGCGGGTGGCGCAGCACCGCGAGCTAACGACGCTAACGACGCTAACGACGCTAACGACGCTAACGAC
 CCCGGTACCGTAGTCGCCGGTGGCTCGCGAGAAAGTGCACCGCCACCCCGCACCCGCTTGACCGCAGCCAGTAC
 GCCACCCCGGATCGGTTGGCAAGGTAAATTGGTCAATTCCATTGACGGGAGCCGACCCCGCAGCCAGTAC
 CGCCACGACCACGCCGCTGACCCACCACTGTACGAACACCAAGGCAGCCGA (SEQ ID NO. 101)

Clone Rv15

:::::::Rv150SP6.seq:::::::
 ATACTCAAGCTTGGCTTCGCCGCCCTGCCGGTGGACTTCATGACAACGCGGGGCGATTACCCCGCTACCG
 CCAGCAGCATGACGGCGTACCTAACACCGCCCGATGCCCTCGCACGTGCGCTCGATGTGCTCACGGAAATGCCCGGC
 ACCCGCATCTCGAGGATCACCGCGTACCCCGGCCAGCGCACACCGACAATTCCGTACACCGCCACGCCGATCCGG
 CCCTGGGCCAGCTGATTGGAGCTGGCG (SEQ ID NO. 102)

:::::::Rv150T7.seq:::::::
 CAGGCATGCAAGCTTCCACATGTACGGATCCACGAACATCCCGTTGAACTGACAGGTGCGGCCGGCTCGATCAGGCC
 GGCACCTGTTCTACGGGTTACCGAAGATCTTCGGTGCACCTGCCGCCGGCCAGCTCGCCAGTGGCCGG
 GTTGGCCGCCGGCGACGATCTGGCTCCACGGTGGTCCGGGTCTGCCGCTAGCACGATCCCGAGTCGGCCGG
 TCACCCGGGT (SEQ ID NO. 103)

Clone Rv151

:::::::Rv151SP6.seq:::::::
 ATACTCAAGCTTCCAAGTCCAAAGTGTGATCATGGCAAAGAGCTCGACAAAGCCGTAGAGGCCTTCCGACCCCG
 CCGCTCGATGCCGCCGTATACTTCTCGCCGCCAGCCCTGGTGTCAAGGTGCGCAGGGCAGGCCGCTGCT
 GGGGTGCACACCTTGATCGCCACCGCGTCAACGCCGAGGGCTACCGAAAGATCTGGCATCCAGGTACACCTCCGCC
 GAAGACGGGCCGGCTGGCTGGCGTCTCCCGCACCTGGTCCGCCGGCTGTCCGGGTCCGCTGGTACCCAGC
 GACGCCACGCCGGCTGGGCCGATCGGGCCACCCCTGCCGAGCCGCTGGCAGCGCT (SEQ ID NO. 104)

:::::::Rv151T7.seq:::::::
 CAGGCATGCAAGCTTACACGTAGGCCGCTGCCCCGTGAGGAGGCCGTTTGGCGTGCAGCCACTGCCGACACCTCGGGGGTA
 AGCGAATCCGAGAGCAGGAGGACGAGGTACCGAAGGCTGCGCCAGCCGGCTGACCGCTCAGGGGGATGCGCCGGTC
 CGCCACCCCGCTACCGCCGATCGGACACCTGTATGACCGCGGCGACGTC (SEQ ID NO. 105)

Clone Rv152

:::::::::::Rv152SP6.seq:::::::::::

CGCGCGGCCGATTACCCCGCTACCGTCAGCAGCTGACGGCGGTAGCGAACACCGCCGGATGCAGCGCAGGTGCGCT
CTATGTGCACACGGAATCGCCCCGGCACCGCGATCTCGAGGATCACCAAGTGCCTGCCCCCTG (SEQ ID NO. 106)

:::::::::::Rv152T7.seq:::::::::::

GGGATCGAGGAACAGCGCGTTGAACGTAGGTGCGGCCGGCTCGAGCAGGCCGCTTGGTCATGCGTTACCGAAGATCTCT
GAAGATCTCTCGGTGACCTGCCGCCGCGCCAGCTGCCAGTGGCGTTGGCGCCGCGAGATCT
GGCGTCCACGGTGGTGGGGTATGCCCGCGAGCAGGATCGCGAGCGCCGGTCAAGCGGGTGAACCTCGAGAG
CTTGACCCCTGCCGTGGGGAGGCGAACACGGTCGGTGCATCTCGACCAAGGCCGGAACCTCGGGGTGGCGC
GACGGTGAACAGGTTGCGCTGGCCACCGCGGGTAGCCGCCGACTATGCCATGCCAGGCCGGATCACCGGTG
GGTCAGTCGGGTAGGATGTCGCCGGCCAGGTGCAAGATCCAGCGGGCGCCGGTGGACACNGGTGATCTC
GTCCACCATCGACTTCTGATCA (SEQ ID NO. 107)

Clone Rv153

:::::::::::Rv153SP6.seq:::::::::::

TAACTCAAGGCTTGCCTGAGGCCAACGGCCATCGACGGTTGGCGCCCTAAATGCACTGAGGTGCGTCAATTGACC
CCACAGCGAAATGCCGACTATTGCGAGGCCCTTCGCTTGGCTGCCAGGGCTCCGCCGGAACCGCATGCA
GGTATATGACCTCGTTCTCGGGTGTACCGCGTGCCTTGTGAGGATGAACTCGCGTTGGAATTGTCAGCCGGC
CCAATTATCGAGCGCAGATTGTCACACATGGCCGGCGACATACGCTCACCGTGGATCTGCTCCACACGGACCG
CCCTGTCGGGATCTGCTCACGGTAAAGGAACCTACNTGGCCTCGGTGCC (SEQ ID NO. 108)

:::::::::::Rv153T7.seq:::::::::::

CCTTCTGCGCACCCACACCGTCAACGCCGCGAAGTCGACGTCCAGGCCATGGCGGCCACGGATGGATTG
GCGCGGACGTGGTGTACCGCGTCCGGCACCGGAAACTACAGCAGGCCCTACGCCCGCATCGCCGG
CCGTTGTGCTGGTGGGTGTGCCGACGCCGACATGCGCTGGACATGCCGCTGGTCGACTTCTCTCACGGCGTG
CGCTGAAGTCGTCGTGGTACGGCATTGCGTCCGGAAAGCGACTTCCACGCTGATGACCTTGACCTGCGATGG
GGCTGCCGCTGCAGCGGTTGTTTCAACGCACTGGCTCGAAGACGTCGAGGAGGCGTTCCACAAGATGCGATGG
GCAAGGTATTGCGTTGGTGTGATGGCTGCCATCGAGCGCTCATCACCCACGG (SEQ ID NO. 109)

Clone Rv154

:::::::::::Rv154SP6.seq:::::::::::

ATACTCAAGCTTGTATTTGATCATGATGATCATCACCCGAAGTGTGGTAGCCGAGTGGTTATCGTGGGTACCGT
CGTGCCTTCATGGGCCCTTCCGGCTTCCGTATTGGCTGGCAGGACATTCTGGTATCGAGTTGACTGGAT
GGTGGTGGCATGTCGGTGTACCTGCTCTGGGGATCCGACTACAATCTGCTGCTGATTCCGGTTGAAAAAA
AGAAATTGGGCCGGATTGAAACACCGGAAATTACCGTGCCTGGCTGGTACCGGGGGAGTGGTTACCGCTGCCGGCAT
GGTGGTCCGGCTTACCA (SEQ ID NO. 110)

:::::::::::Rv154T7.seq:::::::::::

ATTGNCTTCCGGCCATCGGTGAGGACGGCGTGCCTGCTCAACGACGTGTCGCCGGACACACCTCGATGC
TCCGCCATGGACCGGTGCAACGCAAGCAGCTGATCGAGCTACACGCCGCGAACGCTTCCGCCGGCGTG
CCGCATCCCGTTGACCGGGCGATCGCGTGATCGCTGATGACGGCATGCCACGGAGCGACGGCAAGCGCGTG
CCAGGTCGCCGGCGCACGGTGCAGCAAGGTGGTGTGGCGTCCGATGCCAGACGACATCGTGGCAGATT
CGCCGGGTACGCCGATGAGGTGGTGTGTTGGCGACGCCGGTGTCTCGCCGCGGGCAGGGTACCGCAACTT
CACCCAGACCTCCGACGAAGAAGTGGTGGCTTCTGGATCGTGTCTC (SEQ ID NO. 111)

Clone Rv155

:::::::::::Rv155SP6.seq:::::::::::

ATACTCAAGCTTCCCGTCCGTATGCCAACGCGCGTGGCGAAGCGGCTGGTTACGACTCCCTGTTGTGATG
GACCACTTCTACCAACTGCCATGTTGGGACGCCGACCGCCGATGCTGGAGGGCTACACGCCCTTGGTGCCTG
GCCACGGCGACCGAGCGCTGCAACTGGCGCTGGTGGCGACGGCAATACCTACCGCAGCCGACCTGCTGGCAAAG
ATCATCACCAACGCTGACGTGGTTAGCGCCGGTGCAGCGATCCTGCCATTGGAGGCCGGTGTGTTGAGCTGGAAACAC
CGCCAGCTGGCTTCGAGTTGGCACTTCAGTGACCGGTCAACCGCTCGAACAGCGCTACAGATCCTCGAGCCA
ATGGTCAAGGGTGAGCGCAACGTTTCCGGGATTGGTACCCACCGA (SEQ ID NO. 112)

:::::::::::Rv155T7.seq:::::::::::

CGGCCACCGGGCCACTCCGACAAATCTGACCGACCAAGATCTACACCATCGAACGACGGCGTCGCCGACTTTC
CGCGGTACCCGCTCAACTTGTGTCGACCCCTAACGCCATTGCCGGCACCTACTACGTGCACTCCAACTACTCATCC
TGACGCCGGAACAAATTGACCGAGCGTTCCGCTGACCAATACGGTGGTCCCACGATGACCCAGTACTACATCATTC

GCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGAAACCCACTGGCGAACCTGGTTCAAC
 CAAACTTGAAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCTATGTTATTGACCTCGCCGCCAATGTTGCGA
 CTCCGTTGGGTTGTTCCAGAGGTCAAGCCGGTCGTATCGCCGACGCTCTCGTCGCCGGGACCAGCAGGAAATCGG
 CGATTCGCCCTACA (SEQ ID NO. 113)

Clone Rv156

:::::::Rv156SP6.seq:::::::
 ATACTCAAGCTTGGGTGGCCTGTCGGTCGGTGTGCTTGGCGCGTCGGTATCAACACCGCCACGAAATGGGCAC
 AAGAAGGATTCGCTGGAGCGGTGGCTGTCCAAAATCACCTCGCCAGACCTGCTACGGGCACTTCTACATCGAGCAC
 AACCGTGGCCATCACNTCAGGGTGTCCACACCGGAGGACCCGGCGTCGGCGGGTCGGCGAAACGTTGTGGAGTT
 CTGGCCCGCAGTGTATCGCGGCTTGCCTCGCCGTTCAATTGGAGGCCAACGGCTGCGTCGGCTCGCGTCAGC
 CCCTGGAATCCCATGACGTATCTGCGCAACGACGTGCNAACNCGTGGGTATGTCNGTGGTGGGTGGG
 (SEQ ID NO. 114)

:::::::Rv156T7.seq:::::::

TGCCGACCGCACCGCGGAACGCTCAAAGGCACCTACTGGCACCAAGGCCCCACACGTACCCGTGACCTCCTCGC
 CCGACCCCGCCCGAGGTCTGGCGTTACCAAGGAACGGGAGCCGGAGTCTGGTACGCATCGAACAAAAGAGCAAG
 GTGCATGGGCGGAGTTGTCCGCCACTTCGTCGATGACGGGGTCGATCCATTGAGGTCCGTGCCGCGTCGGTCGAG
 TGGCGGTACACTCCAGGTACTCGACCTCACAGACGAGAGGACTCGATCCCCTAGGTGTGGACGAAACAGATCTTC
 TGTCCGACGACTACACCACCCAGGCCATGCCGCCCGCGATGCCAACTTCGACGCCGTACTGGCCCGGG
 CGCGCTCCCCGGTTGTCAAACACTTGGCGTGGTCGTCACGCACTGCCAACATCGAGCCGA (SEQ ID NO. 115)

Clone Rv157

:::::::Rv157SP6.seq:::::::
 ATGAAATAAGAAGAGCACATCCCTCAGTCGGTTATCATCACTAGCGCTGCCGCACCCGTGTAACCGATCATAGCGAG
 CGAAGTGGCGAGGAAGCAAAGAATATCTGTTGTCAGATAGCTTACGCTCAGCGCAAGAAAGAAATATCCCCCGC
 GGAACAACACTCCAGGTAGAGGTACACACGCGGATAGCAATTAGTAATAAAACTGTGACACTCACACCCTCATCAAT
 GATGACGAACTACACCCGATATCCGGTCACATGACGAAGGGAAAGAGAAGGATATCATCTGTGACAAACTGCCCTCA
 AATTGGCTCCTTAA (SEQ ID NO. 116)

Clone Rv159

:::::::Rv159SP6.seq:::::::
 ATACTCAAGCTTGTGAACTCCTTCTGAATACCGCCGGCATCCACAGATGCCCGAAGAACCTCCAGGTACCCAT
 GGCGGCTGGATCAGGGGGCGGCACAGTTGGTCTGTCCTGCCTCGAGTGGCGTGTGTCGGCTTGGACGGGCTCC
 GACGGTACCGGAGGGCAGCGACAAACACTTATGCACTTGGCGACCCGCCAGACGGTGCACACCCATCCGACGG
 CACAAGCTCAGCCGCCGCTTGTCTCGGATCGACATTCAACCACTTCTGACCGGCTTGGCGAAGGAA
 GCAGAA (SEQ ID NO. 117)

:::::::Rv159T7.seq:::::::

GGTATAGTCGCTGACCGGTGCAAGGTTTCGACAATGTTGGTGCCTGGCGCTACGTGCCATCGAGACACTGGCGCA
 GGCTATCGCACCCGTTATCGGCTACGAGCAAATCGGGTATGCGTTCTGAGCATGAGTCGGCGACCGTGTGTCATGGT
 CGACACCCACGAGCGAAAGACGCAAGATCGCCGTCAGCATGTGTGCCCGGATTATCAGGACTGACCTCTGGCTGAC
 CGGCATGTTGGTCGCGATGCCCTGGCGCCGGCGTGGTGTGGCTGGCTCGGATAGCGAGGTCAAGCGAAATTCTC
 GTGGCAGCTCGAAAGGGTCTGCCGGTCTTGCACGATGGCGCAGGTTACGGTGCAGGGGGTGC
 CCTGGCGGGCCA (SEQ ID NO. 118)

Clone Rv15

:::::::Rv15SP6D2.seq:::::::
 GACACTATATNACTCAAGCTCAGGTCAATGTCGCAAGCCCTGACGCTGGCGACCAGGCCACGCCCGGGAN
 CCCTNTCTAGA (SEQ ID NO. 119)

:::::::Rv15T7.seq:::::::

CTGTAGCCACCTGTCATCCCGTCACTGCCGACTCTGGTATCTCGGATCCGTCAGACCCGCTAAGGCTGCTC
 CTCTCGGTGCAATTACCTCACCGACGGCGAACNCCCCAGCTTACGACTATCCGGATGACGGCACCTGGTGTGG
 AACATTACCGTCAGCTGGACGGCGCCTACCGTCGATGGCGCAGCGGGGGCGATGGCCGGGGCGACCGATT
 GTCTNCANCCGTGCGGTGAACCTGGCGACGTATCGTGGTGTGGGCACCGTGCCTGCGCATTGAGGGCTACTCCGGC
 GTCCGGATGGGTGTGTCGTCAGCGCCCGACCGGCAGGCCGA (SEQ ID NO. 120)

Clone Rv160

:::::::Rv160SP6.seq:::::::
 ATACTCAAGCTCGCACGCTCGCGCGCGGTACCGCCCAAGGTGCCCCAACAGATCGTCATGTTCGCGTCGTCCGC
 CTCGCGCACGTGGTCTGTCAACGTTAACGCCGCCACATGTCCTGCGGCCGGCAAAACGTAAAAACG
 AGCGGGCGACTGCNATGTCATGACACCGACGGCCGCCATGGGCCAGGGTCTGGCAAATTGATCTGTGCGGCCAGT
 GCCAGCAGCGTCGCCCTCGTCATACGGCCGGCGACGAGTTGAACCGACATGGGCAGGCCGTGCCGTGCAAGTCCCAC
 GGCACCACGGCGCGGGCTGGCCGGTCAGATTCCAAAATTGAAAGTACGGAACCGCTGCACCACCA (SEQ ID NO. 121)

:::::::Rv160T7.seq:::::::

ATCGTTTCGACCAGGCCTCCATCCGGCAGTGGATACTCCCAGCAGGTAGCAGGTGCCACCACGCTGGTCAGTGC
 CGTCAGCTCGCTTGCAGGCCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCGCAGCTTGGGGATCGCAGCTCG
 ATGGTTGCGGACGGGTGTCGAAATCACGGTGGCGGTAGCCCTTGCCTGCGTATTGGACCGCTCATCGCTGCGTTGCGG
 TAGCCCGCCCCCAGGGCGTCGGCTTCAGCCCCATCAAGGCAGGCGATGAACGTCGAGAGCAGGCCGCGAGCAGA
 TCCGGGCTCGCTGTGCGAGTTGGTCAGCAGAAGCTGCTCGGTGTCGATAAGATGANAAGAAGTCATTGCGTTATTT
 CCT (SEQ ID NO. 122)

Clone Rv161

:::::::Rv161SP6.seq:::::::
 ATACTCAAGCTGGGTGTTGCCGATCACCGGAAGCCGATGATCAGCCACGTTCGCGCCGCCGGCATACGGCGCG
 TACCGATCTCCGCTCATACACCCGCGGTAATCGCGACGGTGCCTGCGAGCCGAAGGTGACGACGCTGATTG
 AATCGAGTTCCAGGTCCAGCGGGTGGCGCAGCAACGGCGAGCTCAACNACGTCAATCACGTTGCTGCTTCTACGG
 TCACCGACCCGGTACCGTAGTCGCCGGTGCCTCGGCCAGAGTTGCACCGCCACCACCGCGACAACGCTTTGCA
 CGCGGACGCCACCCCCCGGAT (SEQ ID NO. 123)

:::::::Rv161T7.seq:::::::

GCGCNAACAGCTCGCGCAGCCACGACGTGCTCGCTCGGATTGCCGGGGCGAGATCAATTCCAGGCAGCTCCCGGA
 CAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTCCCCGGTGCCTGCGAGCTGCGATCGC
 ACAGGTTGGCCACAAACCGGGCGCTTGTGATGCCCTGCGCTGATCACCTACCATGGCCAGGATCTGCGTGTATCACGACGCTCG
 GCTCGCAGTTGGCGAAAAAGTGGCTCGCTGATCACCTACCATGGCCAGGATCTGCGTGTATCACGACGCTCG
 CAAGGGAGGTTGTGTTGCTATGACGGCTTTAGCCAGATGTTGGAAATCGACTATCCGATAGTGTCCGCGCAAT
 GGACTTGATGCCGGCGGTGAGCTGGCTGCCGNGT (SEQ ID NO. 124)

Clone Rv162

:::::::Rv162SP6.seq:::::::
 ATACTCAAGCTTCTCCGATACCGCCATGTCGCGCACATCCAGGACTTCTGGGGGATCCGCTGACAGCGCGGGGAT
 CCCAAAGTGCGGATGATCGGGCCGCTACGTCGTTGTAACCTCGTGGTAACAACGAAACCGAAGCGTATGACTCGG
 TCCACCGGTGCCGCACATGGTGGACACCACACCGCCACCGGCAAGGGCTATGTCACCGGTCCGGCAGCAC
 TCAATGCCGACCAGGCCAGGCCAGGCGAAACAAAAGTATCGTAAGGTACCGGATCACGAACATGGTATCGCAGCAA
 TGTTGCTAGTGTATCGCTCCG (SEQ ID NO. 125)

:::::::Rv162T7.seq:::::::

CCATGAGCACGCCAGCCAGCAGGAGCAAACCTCGCCGACGCAGGCCGGTTGGACTTGTGCTGCTGGACAAGGGG
 TTTAGCCGCCAACAGCAGTGTGACGTACATCGCGAAGAGCAGTCGCTGCGACCGACGGCGCAACCGTGAAGGCTAGG
 GAAGCAGGAGCACATGGCCGCCACCCGCAATGTACACGCTGCAAGCAAACCATCGAACCCGGATGGCTATACATCA
 CGGCCCATCGCCCGGTCAAGCCGGATCGTCGATGACGGCGCAGTACTGATTCACTGCTGCCGGTGAATGCCGACCC
 CGGGAGCACTTCCGCAAAACTAACCGGTTGG (SEQ ID NO. 126)

Clone Rv163

:::::::Rv163SP6.seq:::::::
 CGGGTGTCTGGCCACCGCGCGCGCTGTCCGGGAAATGGCGGGTCCCCGGTGGTTTGCTGAGGAGTGTGAACCG
 TAGTCGAAGTGGCGGGCTCAGACTCCACCCAGCCAGCAGGCCAGCGCAANCTGAATCCTCAACCGGGTTGTCNATC
 CGGACAGGTTGGGTGCGTTGGGCCATNACAGGTGGCGGGGTGCGTTGGGTGGCCGGCGGAGGTGCTGCNTTG
 GGATCCCCGGCTGGCATCGGCNTGTTGGCGGGCGGTGGTGGGGGGCAACACGTGTCNCCTGGTGCCTGGTGGC
 CCT (SEQ ID NO. 127)

:::::::Rv163T7.seq:::::::

CCAAGATCTACACCATCGAATACGACGGCGTCCGCACTTCCGCGTACCCGCTCAACTTGTGTCGACCCCTAACG
 CCATTGCCGGCACCTACTACGTGCACTCAACTACTTCATCCTGACGCCGGAACANTGACGCGAGCGTTCGCTGA

CCAATACGGTCGGTCCCACGATGACCCAGTACTACATCATCGCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGAT
CGGTGCCGATCGTGGGGANACCCACTGGCGAACCTGGGTTAACCAAACCTGAAGGTGATTGTTAACCTGGGCTACGG
CGACCCGGCCTATGGTTATTGACCTCGCCGCCAAATGTTG (SEQ ID NO. 128)

Clone Rv164

:::::::::::Rv164SP6.seq:::::::::::

AGCTTCCCAGAGTCGGCTTGGATCAAGACCCCAGTCGGCGGGCGCGATCCGGCNGCTCGGTGACTACATCAAGCCAC
AAATCGACGGCTTCGGGGTGCCTACCGATGACGTGGGGATGTCGAGTGTGAGTTCTCGGCGGGGGATGCTC
ACCTGGCGATCACCTGCCCTCGTTGACGATCGATCGTCTATGCCGCCGCTCTGCCGGAAACAGGCCNCCAGTACATC
GCCACAGACGGGATCCACCCGCAATTGGCTACGGTTGCTCGTTGAGGACTAGTCGGTCCCTGGTACGTGC
CGGTGATGCGGACCGGTCTAGCACTGACCAATGGCCAAATGCGGGC (SEQ ID NO. 129)

:::::::::::Rv164T7.seq:::::::::::

CGGGGGGCCCTTAATAGTGTAGGAAAGAAGCTCTACATATTAGGAGGATTCAACATGGCTCGTGCCTGGGATCG
ACCTCGGGACCACCAACTCCGTCGTCGTTCTGGAAGGTGGCGACCCGGTCGTCGCGCAACTCGGAGGGCTCCA
GGACCACCCCGTCAATTGTCGCGTCGCCGCAACGGTGGGTCTGGTCTGCCAGGCCAAGAACCGGAGTGA
CCAACGTCGATCGCACCGTGCCTCGGTCAAGCGACACATGGGAGCGACTGGTCCATAGAGATTGACGGCAAGAAAT
ACACCGCGCCGGAGATCAGCGCCCGATTCTGATGAGCTGAAGCGCGACGCCGAGGCTACCTCGGTGAGGACATTA
CCGACGCGGTTATCACGACGCCGCTACTTCATGACGCCAGCGTCAGGCCACCAAGGACCCGGCAGATGCCG
TCTCACGTGCTGCGG (SEQ ID NO. 130)

Clone Rv165

:::::::::::Rv165SP6.seq:::::::::::

ATACTCAAGCTTCATAACAGGCCTGTTGTTGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGC
CGCACCGCCGGCATCTCCCGGTCAAGCAGGGCCGCGGCCGCGCAGCGACGGCTGTTCGCGCAGTTGCCGTCA
ATGATGCTGACCTGATGCCACCCGGCGTTCTCGCGCTTCGCGTTCACTAATCGCGTGCAGCAGCGTCTCG
ACAGCCACCAACCGAGTGGCACCAGCTGCTCACCACGGACCGCAGCGATGCCGTACCTCACCGTCCAGCGGTCC
ACCACGACACGGTGTGACCGCAGCGCGGGATTCAACCACCCAGGGCGTACCGCCAGGCCATGCCACACCGC
ACCATCCCCGATGCGAGCCAGGCCGGAGTAAGA (SEQ ID NO. 131)

:::::::::::Rv165T7.seq:::::::::::

CTGGTGTGGACGGAGCCTAGTACAACCTTCCTCTCCAATGCTTTGCCCGATGCCGGCACCAAGGATGCCAGGAC
ATCTGCGCCCGAAGTACTGGAAAAGCTCACACCCGAGTTGCTCGCACCGGTGGCTACCTGTGACCGAGGAG
TGTGCCACAACCCATGGTGTACGTCGTCAGTGGTGGTTAGGTGAGGCTGCGTGTGGCAACGACGGCGCC
AACTTCGACAAACCGCCGTCTGNTACAAGATGTTGGCGCGGTGGCCGAGATCNCGATCTGTCGGTGC
GCTGGATTCAAGTTGAGAACTAAAT (SEQ ID NO. 132)

Clone Rv166

:::::::::::Rv166SP6.seq:::::::::::

ATACTCAAGCTTTCCGGCGTCGTCCACCTGACCAAAAGCGCAGGTGCCGCCAAACGGCCGCTGCCCGC
ACTGGTCGGCGTCGCCGTGGCGACAATCAGTAGCTGGACATCCGGAAACCGCTGCACCACCTCGGAGCGCGTCAA
GAAAAACGGCCATTCC (SEQ ID NO. 133)

:::::::::::Rv166T7.seq:::::::::::

TTTCAGATCTCATTGACATGACTGGAGATCTGCTAGATTGCAAGCTCTGTGAGCGTGGGTACCGGATTCAAG
CGGTGCGTCACGCCGCGTGGTACCGGCTTGGCGCAGTGCCTCGGCCGAGTTGCCGATCGCGCGAAGTGC
TTCGCGCACCAAGATCGCGGCTAATGGCCGGCATGACCGCGATGACCGCAGCGCGATCCAGGAAAAACCG
AGTGCCTGGCGGCCATCCCG (SEQ ID NO. 134)

Clone Rv167

:::::::::::Rv167SP6.seq:::::::::::

ATACTCAAGCTCCGACACAAAGTGAACAGCACCGATTGGCGAGCACTTCGTCACCTCCAGGGTGCCG
AAGTATTTCGACAAGTATTCCGTCGGGCCGCCGCCGCGCGCAGGGTGGTCATCCTGCCGGGGCTGGAC
TCCCGCGCTACCGGCTGCCCTGGCCGACGGGACCACGGTTTGAGCTGGACGCCGCAAGGTCTTGATTCAAG
CGCGAGGTGCTGCCAGCCACGGTGCCAACCGCGGCCGCGA (SEQ ID NO. 135)

:::::::::::Rv167T7.seq:::::::::::

GTGTGCTGTCAATTGAGACTGAGCTGAGCTGACTCAACTTACTGAGCATGCTAACGCTGGTGTGCGGGCTTGT
CCGCGTGTGGCAGGGCACACGCTGGGGCGTAGCTGGAGAGGCCCCGGTCAAGCCGGAGAGCAGTGCTCAGTCCG

CCAGCTTGACCGACTTCGATGAGAACGCGCTTCGCGTATTGAACCTGGCGTGCCTGACGGTCGCTGAGCAGCGCTC
GCCAGTGCGGCCGCTGATTCTTCATCGAGCCAGGAGGCCATTGCGTGTTCGGCCGCTGCGGGTCGGCCCATCGT
CGACCGCAGTCGTCACCCACTCCTCGATCAGGCTGCGCTCATCGAACGGCAACGGTGTGTCGGAGTATGTGCG
TGGGCACGGCGAGCCGGGTGCTGTGGTACACCCACCGTTGATGACCAAGTTGACGCCTGACTGGCTGAGCACCGCGA
TCCGCTCACAGGTGCGAACGTTGGTG (SEQ ID NO. 136)

Clone Rv169

:::::::Rv169SP6.seq:::::::
ATACTCAAGCTTTGGTCTAGCCGGCCGAGCCCGATACAGGTGTCAATTGCCACCGCCGGCTGTCCGGAAATGG
CGGGTCCCCGGTGGTTGCTGAGGAGTGCTGAACCGTATCGAAGTGCGCGCTCAGACTCCACCCAGCCAGCAGG
CAGCGCAGAACTGAATCCTCAACCGGGTTGTCGATCCGGACAGGTTGGGGTGCCTTGGGCAATGACAGGTGGCG
CGGTGCGTCCCCGGTCCGGCGGAAAGTGTGCGTGGGATGCCCGGCTGGCATTGCGTGTGGCGGCTGCACC (SEQ ID NO. 137)

:::::::Rv169T7.seq:::::::
GGGCCACTCCGACAATCTGACCCGACCAAGATCACCATCGAACGACGGCGTGCCTGACTTTCCGGTAC
CCGCTCAACTTGTGTCGACCCCTAACGCCATTGCCGACCTACTACGTGCACTCCAACCTACTTCATCCTGACGCC
AACAAATTGACCGCAGCGTCCGCTGACCAATACGGTGGTCCACGATGACCCAGTACTACATCATTGACCGAG
AACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCATCGTGGGAAACCCTGGGAAACCTGGTCAACCAAACCTTG
AAGGTATTGTTAACCTGGCTACGGGACCCGGCTATGGTATTGACCTGCCGACCTGACCGAGGACTCCGTT
GGGTGTTCCCAGAGGTGAGCCGGTCTGACGCCGACTCGTCCGCGGACCCAGCACCGAAT (SEQ ID NO. 138)

Clone Rv16

:::::::Rv16SP6.seq:::::::
TTCNTCTCCNNATCGTNNNTCTCTACTACCNGGCCNAAACACCTTGGNAACGCTCAAAGGCNTACNG
CACCAAGGGCCACACGTACCCCTGACCTCCTGCGCGACCCGCCGAGGTCTGGCCGTTACACTGAACGGGC
GAGCCGGGAGTCTGGTACCGCATCGAACAAAGAGCAAGGTGCAATGGCGGAGTTGTTCCGCCNCTTTTTATGACGGG
GTCGATCCATTGAGGTCCGTCGCCGCTCGGTGAGTGGCGGTACACTCCAGGTACTCGACCTNCAGACGAGG
ACTCGATCCCATCTANGTGAGGACNAACAGATCTCTGTCGACGACTACACACCAGGCCATGCCGCCGCC
GCGATGCAAACCTCNACNCCGTCTGGCCCCGGCGCGCTCCCGGTTGTCAAACACCTGCCGTGTTGTTCA
CACTGCCAACATCNAGCCGACNATCCNAGGTCCGTCACGCCCTCCGGCTCNCAAACCTCTCCNCTGATCN
TCCGACCAAACACATGCCGACTCCNTGCNNATTGCTGNATCCCT (SEQ ID NO. 139)

:::::::Rv16T7.seq:::::::
CCGCTATCGGTGGTGTGCTTGGCGCGTCGGTATCACACCCGCCCCAGGAAATGGGCACAAGAAGGATTGCTGGAG
CGGTGGCTGTCAAGATCACCTCGCCCAGACCTGCTACGGCACTTCTACATCGAGCACACCGTGGCCATCACGTC
CGGGTGTCCACCCGGAGGACCCGGCTCGGCGGGTTCGGCGAGACGTTGTTGGGAGTTCTGCCCCGAGTGTATC
GGCGGTTGCGCTCGGCGTTCAATTGGAGGCAACGGTGCCTGGCTCAGCCCCCTGGAAATCCCATGACG
TATCTGCGCAACGACGTGCTCAACGGTGGCTGATGTCGGTGGTTGTTGGGCTGATCGCGGTCTCGGCCCG
GCGCTGATCCGTTGTCATCATCCAGGCAGTCTCGGCTTCAG (SEQ ID NO. 140)

Clone Rv170

:::::::Rv170SP6.seq:::::::
ATACTCATGCTGCCGAAGTCCGATGGTGCCTGCCGGCGANCCCAGCGAACGCTAGCGTGGCGTGTCTGGCT
TCGGATCTATCCTCGTACATGACCGGCACCGTGTGGACGTACTGGCGCCGGTTCATATGACACCGAGATCATTGC
CACGGTACGGCAATTGCTCAAGAAGGAAATCTTCCAATGACCCGCCCTCGAACGTGGCAACAGCTACCCGAAGA
AATCGTCGATCGGCTGGGTGTTATTGCTGCTCGGTGCCGCTGCAAGGGTATGACACCACCGAGTTCATTCTCC
GGCGTGGC (SEQ ID NO. 141)

:::::::Rv170T7.seq:::::::
GGCGTCAACGGTGTGGCACCCGGCGTCTGCAAGTGGTAGGCCGTCAGTTGTCATCAGGCCGATGCCGCCCTC
GTGGCCACGCATGTACAGCACACGCCGCCCTCACGGCGACCATGCCAGCGCGTCCAGCTGAGGCCGCA
ATCGCAGCGCGTACCCAAACACATGCCGGTCAAGCACTCCGAATGACCCGGACCGACGTCGTACCGTCGGC
GTTGGGCCGGGATCTGCCGCCGGACAGCGCAGATGTTCCACGTCGTAGATGCTGGTAGCCGATGCCGCG
AATCTCCCATGACGAGTCGGAATCCGCCCTCGGCG (SEQ ID NO. 142)

Clone Rv171

:::::::Rv171SP6.seq:::::::
 ATACTCAAGCTTCGGCCTCGCTGCAGGAGTGGGAGCCGAGGGCTGAAATCGAAAACGAGCCGGTGATCGCACTGTCGGCAGTCGGCAGCTGGTGGTGTACCGATGAATCCGCACCCAAATGTGGCTGCGGTGGCGTTCTTGACCTCTTGGCGTCGACTCTTGTCGGCAGCCACCGAGCGGTTGGTCCAGGATCTGGATGGCAAAGTTGTGCGGCCGGCGCGTACACCTCAAGCATTCAATGGTTAT (SEQ ID NO. 143)

:::::::Rv171T7.seq:::::::
 ATGCGTCACCCCGATGCGCCAGATCGGGCTTCGCAAATAAAGCACGAACAGGCCAAAACGTCTATCTGGAGCCGAAGGGCAATCAGCCGACCGTCGACGAACGACACCGCGATAACCCTAGGCCTGAAACGCCGGCCAAACATTACGCCCTCCGTTGATAAGGCTTCCGCTCTTCCCGTCATCCCAAGCACCTTGCGGCCAAATTGAACGCTTCCTGTCGGGCACCGGCCCGGGCTTGGGTCNTCCGA (SEQ ID NO. 144)

Clone Rv172

:::::::Rv172SP6.seq:::::::
 ATACTCAAGCTCAATCGGCCGCCACAATCCAAATATGCGTCTAGCGTCTCGATGAGCGTCGGTCCGGCATCGGCTAGGGCCGATCACGCTCCAGCCAAAGGCGTCGCCCCATCAAGGGCGCTCAGGCCAAATTC CCCTATCCAGCACGGGCCGCGCTCCGCNCAGCCGGCACGGCGTTCATCCGGAGATCGCCTCGCTAGCGCTGGTGCAGCATGGCGCCGTGGGCGATGACCACCGGGCGT (SEQ ID NO. 145)

:::::::Rv172T7.seq:::::::
 TTCGGCGGGTCTGTAGATTGCGGTGGCCACCCACAGGCACTCATGAACCGCAGGCCACGATCGATCTGGTGG (SEQ ID NO. 146)

Clone Rv173

:::::::Rv173SP6.seq:::::::
 GCGCACCATGCCAGTAGGTGCCGTGGTGGCGCTCGAGCCACCCGAGCGGAAACGCGAGTCCGAACAGCAACAGCAGGACGGCGCAACCAGGGCGGTGACCATGCCCCGGCGCTGAACATCAACCACAGGAAGGGCTCGCCAGCGTCCGCGACC (SEQ ID NO. 147)

:::::::Rv173T7.seq:::::::
 CATCGCGAACCTCGGTCCGGTTGNTAGNACCGCAGCACAAACGCAACCGACCCACCGACCCCCACGCTTACGCCAACCTTTAGTTCAITGGCGTGAACAGCAGCGTAGCCGGTTGCCCCGATATATGTGGAAAATGTTGGACGTACAAAAAAA GTTCCTGACGCTGGCGTCAACTCGAAACTGCCTCGGAAGTCAATGATGATCCATCAGTCAATATAAGTCG (SEQ ID NO. 148)

Clone Rv174

:::::::Rv174SP6.seq:::::::
 ATACTCAAGCTGTCTGCTGCCCTAGCGTATGCGATCCAAACGCGCATCGCGATCAACGATCAGGCCGCCGATTCGGGCCGGCAGTGGCACTGGCCAGATGGCGTTTTCGAGAAAACCTCAACGCTGAGCGCTGTTCCCATCGAGAGACCGGTGGCCTCTACACCGATGCCAGTTGGACCGGGGATGTTGCCAGCGCCTCACATACGGCAAGTNTGGCGGG (SEQ ID NO. 149)

:::::::Rv174T7.seq:::::::
 TTGTCCAGGCGGGGAATCGGGCAGGGAGACGACACCTTCGTTGATCGTCCGAAACGGTAGTTGGCCGACCACGTTGTTGGGTCAAGCGCTGACTTGCCAGTGGCCAGGCCCAGATCCCCAGGCTCAAGCTCACAGA (SEQ ID NO. 150)

Clone Rv175

:::::::Rv175SP6.seq:::::::
 ATACTCATGCTGGCGCCTGGGTGGCAGCCCACCTGCCACACAGGACCGCGGTGCGGACGCCGGCTGACCGCCCTGTCAGCATCGTGGCCGGCTCTGCTGTTGTATGCCAACTTCCGCCGCAACTGCTGGTGGCCGGTGGTTGGCTCGCGATTCCGCTCGCATTGCTGGCCTGGGTGCTGACCCNCCGCNCACAAACACCGGTGGTGGCTGGCTACGCCCTGCTATTCCGCTGGTGTCTACGCTCTCGTTGTCGGTGGATCGGCAGCTGGTGGGCCCCGGGCTGGTGGCACTGGCAGGACGACGTCNGCGCTGTTGCCACTTCCCGGATCTCGGTCTGTTGCCGCTGTTGACCTGTTGCCGGTTGGCC (SEQ ID NO. 151)

:::::::Rv175T7.seq:::::::

CGCCAATTCAAGATATCGTTAACCGATATCCCGAGCCGATAGCTGGCGGGCTCGGGTGGTGGCCAGCGCGCTGCGACGAAAGGTGTGACCGTCACTGAAACAGACACCACCGCGCCGTCGGCCGTCGTCACCTGCTGAGATCTCAGCATCCGC

AGCCGGTGTGATCGCGCTTCGGCGTGTAGTGGGTGCCGCCGACCCCGGAAAGGCCGGCCGACACAACCCCGGA
ACAGGAAGTCCCGGTACCGCAGCCGAAGNACTGATGCCGAACNCGGAGTGCTCCAAACGATCCTGCTGAT

(SEQ ID NO. 152)

Clone Rv176

:::::::Rv176SP6.seq:::::::

ATACTCAAGCTTGGGCACTGACTTCGGTACCCCTCCGCCCTTGGCCAGCAGCAGGCCACAGCGGGTTCGCCGACCGA
ACGTGGACATCAATAGCCCGAATCGGTGTGCAAGTGTAAACGGTGTGATCCAGCTTGGCAGCCTTTC
TAGCTTGGGCCCCACACCCACAGTGTGACGGTACGGTACCCATGATGCCATCCAGTGGCATCGGTGAGCT
GATAATGCCAGCTGGTTCGCAACCCGGTAGCGATCTGGCGCTGCTTGTGACTGATACTATCGAGCAAG
ACAGCCCGGTTGCGACAAAATGACTTTGGATCTCTCGGACTTCGATGGGTCGTCGGGA (SEQ ID NO. 153)

:::::::Rv176T7.seq:::::::

AAAGTCTGTGCCGGTTCGCTAAACACCCGGGACACTCAGACGGTGTGGTGGTGCAGCAGGCCATGGCACCCGGGGAGC
AAAGCGCACTCTCCGGGGACGACAGCAAGCAGCCAGCTAGACAAGAGGGGCGTGCAGCAGAACGTTGGTACA
CAGCTGCTGGCGTTCGGGCCACCGATGTTTATGCCGCCACCGGGTGCCTGCACAGACGATGGAGCCACTCGCC
CGGAACTGAACGTGACCATACACA (SEQ ID NO. 154)

Clone Rv177

:::::::Rv177SP6.seq:::::::

ATACTCAAGCTTGGGTTCACGCCCGCGCAGCCACGCCGTACCTTCCACGAGACCTCACCGATCCGAAATGG
AATCGGGCTGACGGAAATGGCGCACCGAACACCCAAACGAGGTGGTGGCTCGTGCAGCAGCCGATCGCGG
CCACCGTGCACGGCGACGTTCTACACCCGACCAAGATCCGAAAGCTGCAAGCTCCAGCACCAGTCCGACGTCA
TCACCGCTGCCGCCGGCACGTCTTACCTATTGAGCTGGATCGGCCGCTGGTTGCTGGAGTGCCTGAGGAGTGC
TGGCTAGAACCGGGGGCACACCGCNCCTGGGGGGCGAATTCTTGACCGCNCCGGC (SEQ ID NO. 155)

:::::::Rv177T7.seq:::::::

CGCGGTTGGCGTAGTTGGACGGGTCGCCCTCCGAGGCCAATGATGACGATGACCACGCCGATACGATGGCACCGAG
AGGACAACAACAGAAAGCTGACGAATCCCTCCTTGGCGGCCGGCTTGTGGTGCCTGGTGCAGCAGGCCAAT
TTACGGCCCGCTCCCCCAGGCCGCCAGCCAGGGTCCCCAGCCAGTGGCGTAGGCCGAATTACGATCAGCGCA
CCCGATAACCTGCCATGCCCTGGGCATATCGATGTGCGGCCAGAACAGGCCAAC (SEQ ID NO. 156)

Clone Rv178

:::::::Rv178SP6.seq:::::::

CCAACAAGAGCATCGGACATACGGAGTCAACTACCCGCCAACGGTGATTCTTGGCCGCCGTGACGGCGCGAACG
ACGCCAGCAGCACATTCAAGATGCCAGCGCGTGCCTGGGCCACGAGGTGGTGTGCTGGCGGCTACTCCAGGGTG
CGGGCGTGTGACATCGTACCGCCGACCACTGCCGGCTCGGGTACCGCAGCCGTTGCCGCCCGCAGCGGACG
ATCACATGCCGCATGCCCTGTTGGGAATCCCTCGGGCGCTGGCGGGCTGATGAGCGCCCTGACCCCTCAAT
TCGGGTCCAAGACCATCANCCTCTGAAACAACGGCAGCCGATTGTTGTCNGACGGCAACCGGTGGCAGCGCACCTAG
GCTACGTGCCGGGATGACCAACCAGCGCGCTTGTGCGAGCAGGATCTAACCGCAGGCCCATAGATTCC
CG (SEQ ID NO. 157)

:::::::Rv178T7.seq:::::::

TAANACCCGTGTAATTGGGATGGGCAAAAAGGCCAAGCACCGCGTGGGCCACGAACGCCGGAGGGACAATCTGGGC
GGCTAGGGCTTCTCGCGGGAGGCCAACGTAACGGCGTTCAACACGTCGCTCCGCCACCGCAACATTGG
GGATGGCAGCAACCTGGTAGCNCCCTGGCGGGCGATGATCTGCAGCGTCGCCGGGTAGTCGCCGCCGGCG
ACAGTCTGAAACCGCATGACCATCGATGTGTTGAGCAGCATCCGACGCAACGGTCTACACGGCAGTATGTTGCC
TCGCTGCCGGTGGACGGTGGGTCTATCCGGAGACCGACNTCCCGATCGAAGCGACCGTCTCTCGATGGACGCC
GGCGCGTCACCTGGGTTGCTACCGCCTGGCGTGGCCCCAA (SEQ ID NO. 158)

Clone Rv179

:::::::Rv179SP6.seq:::::::

GTCCGAAAAGACTCAGCGGCCACTTGTGTCGAGCTGGCGTACCGGCCACCGATCGATGCCGTGGTGC
GAATGCCCTCCGAAATCGCACGGCGACTCCAGTGTGGCGAGCATCCGCGATGCCAGCTGCCGGTGC
CACGGCACCCACATGCCGAGTTCGTCACCTGGCCAGCGCCGCCGCCGAAGTCAAACAAATAGAAC
GCCCGCATCGTGGGTAGCAGCCAACGCCATGATCAGCGTCCGAGCGCGTTGACTTGGCGTGC
GACCGCGACATTGCCCTGCCGCCCCGGACAAGTCGATCGTACCGGCACCCN (SEQ ID NO. 159)

:::::::Rv179T7.seq:::::::
 CGTGGCCACGAAACGCCGGGAGGGACANTCTGGCGGCTAGGGCTCTCGCGGGAAAGGCCGAACGTACGGCGTTCA
 ACACGTCGCGTCGCCCTCGACCGCAACATTGGGGATGGCAGCAACCTGGCAGCTACCTGGCCGGGCGATGATCTG
 CAGCGTCGCCGGGTAGTCGCCCGCCGGCGCTACAGTCTGAAACCGATGACCATCGATGTGTGGATGCATCATC
 CGACGCAACGGTCTACACGGCGATATGTCNCCTCGCTGCGCCGGTGGACCGGGTCTATCCC (SEQ ID NO. 160)

Clone Rv17

:::::::Rv17SP6.seq:::::::
 ATACTCAAGCTTGCAGCGGGCGCCAAATGTGAACGCACCAAACCCGCCGCTGGGGTGGCCGGCACTCGACCT
 CGAATTTCGCCCGCGTGCACCATCCAGCCGACGGCAGTTGGGCACCCGCCCGTGCAGCATAACTGTTGGCGT
 CGCCGTCTAAAGCTCGAACAGCACCGAAACCGACTCCACCCGGCGGTGCAGCTCAAATCCACGCCGATCTCCA
 CATACCGGGAAAACGTCGGTGTCCCCTCGGGTTGCGCTTGGCCAGCTGCACACCACCGGTGGCCTGGCACCT
 TCGCGGCTGAGCGCAGCTACNCATCCTGACGATCATCACCCGCCCGCTACGCTTGGCTCCGTGACCGCACG
 CATCGCCCGGTTGCGCGACCGCGACGCCGTACAGCGCGCAC (SEQ ID NO. 161)

:::::::Rv17T7.seq:::::::
 AGCTTGCGGGACTGCGGAACAGAACAGCGGGTTCTACCGCGGTGTGCGGCCGGCGATATCGGCCTTTTACTAA
 CCGAACCCGATGTGGGCTCGATCCGGCGCGATGGCATCGACGGCGACGCCGATCGATGACGGCAGGCTTACGAGC
 TTGAGGGTGTGAAGTTGGACCAACGGTGTGGTAGCGGACCTGCTAGTGGTATGGCGGGTACCGCGCAGTG
 AAGGGCACCGAGGGGAATCAGCGCTTGTGCGAGGCTGATTGCCCCGGGATACCGTGGAGCGGCGAACAGT
 TCATGGGACTGCGTGGCATCNAACAGCGTACCCGCTCATCGCTNGGGGCCAAAGACAACTTGATCGGCA
 (SEQ ID NO. 162)

Clone Rv180

:::::::Rv180SP6.seq:::::::
 CTCAGCTTGGCGATGCGGGCTGGCAAAACTGCCGGGGGGTTGGCTTGTCAATCAAGGGTGGGTGCGG
 (SEQ ID NO. 163)
 :::::::Rv180T7.seq:::::::
 CCGAAGGCCCGTCCGGCGTTAGCAAGCGATCGTCGGTTGGCCACTGCGGTGAAATCTGCGGCCGCGCG
 CGTGGAACGCCAGGTACCCGGCGCGTAC (SEQ ID NO. 164)

Clone Rv181

:::::::Rv181SP6.seq:::::::
 ATACTCAAGCTTTCTGCTCATGAAGGTTAGATGCGCTGCTTAAGTAATTCTCTTTATCTGAAAGGCTTTT
 GAAGTGCATCACCTGACGGGCAAATAGTTCACCGGGTGGAGAAAAAGAGCAACAACTGATTAGGCAATTGGCGG
 TGTGATAACAGCGGTAATAATCTTACGTAAATTTCCGCATCAGCCAGCGAGAAATATTCCAGCAAATTCTAT
 TCTGCAATCGGCTTGCATACGCTGACCACTGTTAGCAGGAAACACGATAATCAGCTTACCAATCTGGATAATG
 CAGCCATCTGCTCATCTCAGCTGCCAACAGAACACGATAATCAGCTTACCAATCTGGATAATG
 GACTCCCATCGGAAATTCTATGACACCAAGATACTCTCGACCGAACGCCGGTGTCTGGTACCA (SEQ ID NO. 165)

Clone Rv182

:::::::Rv182SP6.seq:::::::
 CTCAGCTTGGGCCGACATGGCGGGCTGGAGCCCGGTATGGCAAGGTTCCGCTCAATGTGGTTGTGATGCGAG
 GACTACGTTGCCCTCAATCAGCTAAACGTCAACCCCGTGGCGTGTGCGCAGCATGAAGGTCGGCCGGCAGATG
 TGGCGAAGGCAACAGGTAACAGGTAACAGGTAACAGGTAACAGGTAACAGGTAACAGGTAACAGGTAACAGG
 GCCGGAGTGCCGGTCAACTAACACGCCCTCACCGATTTCTGCTAAAGAACACCCGGGAGATCGCGATCGAAC
 (SEQ ID NO. 166)

:::::::Rv182T7.seq:::::::
 CCGAAGCGTGGGAAATCCTGACCGAACACCCGGAGCTGGAAAGCATCTCGCTGACGTCTAAAGCGGCCGCG
 TGCACCGACCCGAGCTGGAAAGCATCTCGCTGACGTCTAAAGCGGCCGCGCTACCATGTCGACGACTTCGGT
 GCCGGATCCCGTGGACAAACCGCCCATCAAGACACCCGGGAGATCGCGATCGAACACGCCGAAACTGGGCC
 (SEQ ID NO. 167)

:::::::Rv183SP6.seq:::::::
 CGACTCGACAAGCATTCTGACAGTTGGCTGGCATGGTAGCCAAGGTTCTGGTCCACAGATCATCTT
 GGTCCGGTAGCGCTCGTCCGGTATGCTGCCCGGGATTCTCGCTGCTATTACTCCCCCGAAAAACGCCACCGGTC
 CAGCGCGTGGGCCGCCGGTCCCCATCACAAACTGAACCCCAACAGGGACATGCTTAGCGTAGGGCGCGCCA
 AGGCGGAGCAATCGCATCTGCGCTGCGCTCACTATTAAACCCACCCGGACTTCACTTCCACGACCCGAATGGCG
 CCCGGTCAATTGATCATCTGCGCACCGCGGATAATCCGGGATTGCCAGCCATTGACTACCGCATGCGAGTCATCG
 CTGACCGCAGCGGTCCGATTACCGAGCGCCCCGANTACATCTCTCCAATATCAATGGCGCAA (SEQ ID NO. 168)

Clone Rv183

:::::::Rv183T7.seq:::::::
 CGGGTNTAGCTTCCCGTGTACCGGGCACCAGCGAGAAGCTCGTTTCCCAGTGTGCTGGGATTCTCACGCT
 GCTGCTGAGTGCCTGCCAGACCGCTTCCGCTCGGGTACAAACGAGCCGGGGCTACGATCGCGACGCTGAAGTT
 GGTGTTCTCATGGACTTGGGATGTGCCTGAACCGGTTCACCTACGACTCAAGCTGGCGCGTCTGTCCGAGGT
 CGTGCTTGCATAGCCGGAGGGCCGGATCCGCAATGACGGATTCCATGCCAACGCTCCGAGTTGCATGCCGATCGA
 CTACGAATTGATCACCCAGAACCATCGGGCTATTACTGCCTGAAGTACCTGGTGCAGGATCGGATACTGCTATCCGGC
 GGTGACGACCCCCGGCAAGCCGCCATCCGTGCTGT (SEQ ID NO. 169)

Clone Rv184

:::::::Rv184SP6.seq:::::::
 CTCAAGCTTGGCGTGCACGGCACCAGGGGCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATGAATACGA
 CGCGCTCGCCGACTTTCCGCGGTACCCGCTCAACTTGTGTCGACCCCTAACGCCATTGCCGGCACCTACTACGTGCA
 CTCCAACTAACATCCTGACGCCGGAAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGAC
 CCAGTACTACATCATTGACGCCGGAGAACCTGCCGTGCTAAAGCCACTGCGATCGGTGCCGATCGTGGGAAACCACT
 GGCGAACCTGGTCAACCAAACCTGAAGGTGATTGTAACCTGGCTACGGGACCCGGCTATGGTTATTCC
 (SEQ ID NO. 170)

:::::::Rv184T7.seq:::::::
 CGGGTGTATTGGCACCCGGCGGCTGTCCGGGAAATGGCGGGTCCCCGGTGGTTTGCTGAGGAGTGTGACCG
 TAGTCAAGTGGCGCGCTCAGACTCACCCAGCCAGCAGCGAGCTGAATCCCAACCGGGTTGTCGATC
 CGGACAGGTTGGGTGCGTTGGGCAATGACAGGTGGCGCGGTGCGTTGGGTCCGCCGGCGAGGTGCTGCGTTG
 GGATCGCCCGGCTGGCATTGGCGTGTGGCGGCCGGTGGTGGGGGGCACANGTGTGCCGGTGCAGGTTGGC
 GCTGCA (SEQ ID NO. 171)

Clone Rv185

:::::::Rv185SP6.seq:::::::
 NCTTGATATTGGCGTCAACGGTGTGCGCACCGCGTCTGCAAGTTGGTAGGCCTGCAGTTGTGCATCAGGCCGATGC
 CGCGGCCCTCGGCCACCGCATGTACAGCACCAAGCCGCGCCCTCACGGGCGACCATGCCAGCGCGGTCCAGCT
 GAGGCCGCAATCGCAGCGCGTGAACCAAACACATCGCCGTCAAGCACTCCGAATGCACCCGACCGACGCTCGT
 CACCGTCCGCGTTGGCCCGGATCTGCCGCCGACAGCGCAGATGTTCCACGTCTCGTAGATGCTGGTAGC
 CGATGGCGCAGAAACTCCCCATGACGAGTCGAATCCGCCCTCGCGACCCGCTCAATGTGCTTCTCGTGCCTGCC
 GCCATTGATCAAGTCAGCAATGGTGATCAGGCCAGACCGTGCNTCGCG (SEQ ID NO. 172)

:::::::Rv185T7.seq:::::::
 CATAAGGGCCGGCGTACCGGTACCGCCGCGGGCTTACACGTGCCGGAACCTGGAAAGCGCAGTAAGCCCTAACGCG
 CCACCGCTTGGCCCGCGCCGGCGTAGGCGCATCGCGGTGGCGTGGGGCGGCAGTGCACCTCACAGCGG
 CTTTCGAGCTTGTTCGATCAACCGGCCAGCATGGTCGAGGATGCAATTGAGACCATATTGAAATTGGTTCATCGG
 GGGCCCGATCCGATGCCCTCCAGTTGCGTAGCAAGCAGCGGAGTCGTCGGGAGTCGATGGCACGGGTGTT
 CAATGGCGGATGGTCCGCTGCCGCCACTGGCTTGCAGGAGAGCCGATCTAGCACCACCGATCCGCCACGTGGA
 CCGAAACCGCCAGTAGATGTCGAAAGCGT (SEQ ID NO. 173)

Clone Rv186

:::::::Rv186SP6.seq:::::::
 CGTCCTTTCCCCAAGATAGAAAGGCAGGAGAGTGTCTCTGCATGAATATGAAGATCTGGTACCCATCCGTGATACA
 TTGAGGCTGTTCCCTGGGGTGTACCTTCACAGCAAAACACGTAGCCCTTCAGAGCCNNATCCTGAGCAANAT
 GAACAGAAACTGAGGTTTGTAAACGCCACCTTATGGCAGCAACCCGATCACGGTGGAAATACGTCTCAGCAC
 GTCGCAATCGCGTACCAACACATCACGCATATGATTAATTGTCATTGTATAACCAACACGTTGCTCAACCCGTC
 CTCGAATTCCATATCGGGTGC (SEQ ID NO. 174)

Clone Rv187

:::::::Rv187SP6.seq:::::::
 CTCAAGCTTGTCCGTACGGCTCGGGTACGCTTCCGTCGAGTGTGCGAGTGTGATAAAATGACGACCGGGACCTCGTC
 GGCATCTCCATAGCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGTAGAAGGTGCGGAGCGCTCGGCATT
 GGTGATCGGGATATGCCGCTCGGGACGGTCAGACCCCTCGGGTCCGCCAGCACTCCGAGGCTCGTGGGGTGGTC
 GCGACACGCATGGGCCACCATCGCATTCA (SEQ ID NO. 175)

:::::::Rv187T7.seq:::::::
 NCGCCGCCAGCCACCACGCCGGGTGGCGCCGGGGCCAGGCTGCTCCGCTGGTATGGCACGCCACC
 GCGACACCACCCGGCTCGCTACGTCGAGCCATACCGGGGGAGCTACATCGGCTGGCGCCAGTGTTCGGGCCT
 CTTTCGAGGTCGAGGTCGATACCGATTGCGCATCCGCAGCCGACCCCTGGACGACAGAACCGTGCCTACGANTGCT
 TGTCGGGCGGGCAAAGAACAGCTGGCATCTGGCGATTGGCCGGCGCTGGTCTCAAAGAACAGGCC
 TTCCGGTGTGAT (SEQ ID NO. 176)

Clone Rv188

:::::::Rv188SP6.seq:::::::
 CGCCACGTTCATGGCAACAACCCGATCACC GGTTGGAAATACGTCTTCAGCACGTCGAATCGGTACCAAACACAT
 CACGCATATGATTAATTGCTCAATTGTATAACCAACACGGTGTCAACCCGTCCTCGAATTCCATATCGGGTGC
 GTAGTCGCCCTGTTCTGGCATCTGTAGCCTGAGAAGAAACCCAACTAAATCCGCTGTTNCCTATTCTCC
 AGGCCGGG(SEQ ID NO. 177)

Clone Rv189

:::::::Rv18SP6.seq:::::::
 ATACTCAAGCTTCAACC GATTGACGATTGTGCGAAGTGCAGGGGCCCGCATGCCAATCCGGAAGACCATCATTG
 GCCAGTGGCCGGGCGCTAACAGGTTCCAGCCCCCACCAGTGCCTCGAACATGCCGTTGCAACCCATTGCAGGCC
 GCAGGGAAAGCACCGCGGAAGCCGCAAAGGGCTGCAGTCCCGGCCAATAGTGTGTCGGCAACCAGATGCCGCTGA
 AAACCGCGCCGGCAGTCAGCGCACCGACGCGAGGTCGAGAGACGTCGTCAGCGGCCACATGGGGTGC
 ACAGCAGGTAGGCCGCGCAACCCGAAACGCGTGGTGCATGCCACGGTCCGAGGAGGCCAGCACCCGCAATGCC
 GAAGCCCACGAAACATGGCGCATCCACGCTTCAACCTC (SEQ ID NO. 178)

Clone Rv18

:::::::Rv18T7.seq:::::::
 AGCTTTGGCAGGGTCTCTCGAATTGGCGTGACCGCTATGGTTGCAGCACGGCTGGCGCCACACCCACT
 GGCCCGGGTGTTCGCCCCAACCGGATCATGGTGAGCGAAAAGGAGATTGCGCTTGTGATGCTGGGATTGCGCA
 CCCGAGGCCATCGACC GATTACTGCCACCGGGGTGCGAGAGGTGCGCAGTCCGCTCCGTGACGTCTCCGACGA
 TCCATCCGGCTTCCGCCGTCGGGTGCGGTAGCCGTCGATGAAATCGCTGCCGGCGTACCCACAAGGTGATTCTGTC
 CCGTTGTGTCGAAGTGCCTTCGCGATGACTTCCGTTGACCTACGGCTGGGGTGTGGCACAACACCCGGTGAG
 GTCGTTTTGTTGCGAGTTGGCGGAATCGTGTCTGGGTACAGCCCCAATCGTCAC (SEQ ID NO. 179)

Clone Rv190

:::::::Rv190SP6.seq:::::::
 ATACTCAAGCTTGTCAACCAACTGTTCCACAGGGCCTCCATCCGGCAGTGGATACTCCCAGCAGGTAGCAGGT
 CGCCACACGCTGGTCAGTGCCTCGGGCTGCAGCAGCCAGTCCGGAAATAGCTGCCCTGGCG
 CAGCTGGGGATCGCAGCTTCTATGGTTGCGGACGGGTGTCGAAATCACGGTGGGGTAGCCGTTGCGCTGATTGGA
 CCCGCTCATCGCTGCGTTCCGGTAGCCGCCAGGGCGTGGCTCAGCCCCCATCAAGGGCGGATGAACGT
 CGAGAGCAGCCGCGCAGCAGATCCCCGCTCGCTGTGCGAGTTGGTCAGCCAGAACCTGCTCGGTG (SEQ ID NO. 180)

:::::::Rv190T7.seq:::::::

CCTTAAGCCCCGAGGGCCGGCACGCCGGTACCGCCAGGTGCCCCAACAGATCGTGATGTTGCGCTGTCGGCC
 TCGCGACGTGGTCTGTACCGACTAACGTTAACGCCGCCACATGTCCTGCGGGGGAAAACGTGAAAACGA
 GCGGGCGACTGCAATGTCATGACACCGACGGCCGGCATGGGCCAGGGTCTGGCAGATTGATCTGCGGCCAGTG
 CCAGCAGCGTCGCTCGTACACGGCCGGCAGGAGTTGAAACCGACATGGCAGGCCGTCGGCTGAAAGTCCACG
 GCACCAAGGCCGGGGCTGGCGGTAGATTCCAGACTTGAAGATCGGAACCCGCTGCACCAACACCAGCAGAACGTG
 AAACTGCACCCGGCGTTGGTAGGCCGATGCGGGACGGCCGGTCCGCGCTGGCTCACAAACTACGTCGACAT
 CGTCGAAGATCGACTGGATCGCTGTCACACCACCGCCGAGGCCACATCCGCGTC (SEQ ID NO. 181)

Clone Rv191

:::::::Rv191SP6.seq:::::::
 AGCTTTTGAGCGTCGCCGGGGCAGCTTCGCCGGCAATTCTACTAGCGAGAAGTCTGGCCGATACGGATCTGACCG
 AAGTCGCTGCCGTGAGCCCACCCCTATTGGCGATGGCGCCGACGATGGCGCTGGACCGATCTGTGCCGCTTGCG
 ACGGCGACGCCGGTGGGTGGTCAAGTCCGGTCTACGCTTGGCCTTGCGGACGGTCCCGACGCTGGTCGCGGTTGCG
 CGCGAAAGCGCCGGTGGGTGCCATCAGGAATGCCACCGCCGCGACTGCACGGCCAGTGCAGGCCGATGTCA
 GCCATCGGGACATCATGCTCGCTCATACTCCTCGACCGAGTCGGCGAACAGCTGATTCCCGGACCGCCAGCGCA

TTGGTATGGAATCGCGAACCTGGCACCCGCTGGTGTGACATCCTGACGGTGGCAATTGCCCGTAACGT
TTGCCGCT (SEQ ID NO. 182)

:::::::Rv191T7.seq:::::::
CGGTCCGACCCCTGTCGACGGCTACCTGAATCAACCGATGCCACCGCCGGCGTTCGACGCCGACAGCTGGTACCG
CACCGCGACGCTCGCGTGGTCGACGGCAGTGGATGACCCGATCGTGGACCGAGTCGGTCGACTTGATCAAGTC
GGTGGATACCGGGTCGGCGCCGGTAAATTGAAACGGTGTGCTCGGCATCCGGACGTGGAGGCGGAGTCGT
CGGGGTGCCGACGATGATCTAGGCCAGCGGATCGTGCCTACGTAGTCGGCTCAGCGAATGTCGATGCGACGGGCT
TATCAACTTTGTTGCCAACAACTTCGGTGACAAGGCCCGCGCAGGGTGCATCGTANATGCGCTGCCGCAA
CGCCTGGGAAAGTGTCCAGAACATTGCTGTCAGAAGCTGANCTACCGAATTATCGTGTACGCTGGA
(SEQ ID NO. 183)

Clone Rv192

:::::::Rv192SP6.seq:::::::
ATACTCAAGCTTGGCGAACGGTCCGATGGGTCGCCGGCGAGCCAGCGAAGTCGCTACCGTGGCGTGTCTGGCT
TCGGATCTATCCTCGTTCATGACCGGCACCGTGTGGACGTGACTGGGGCCGGTCCATATGACACCGAGATCATTG
CACGGTACGGCAATTGTCAGAAGGAAATCTTCCCAATGCAACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGA
AATCGTCAATCGCTGGGTGTTATTGGCTTGCTCGTCGCCGGCTGCAAGGGTATGACACCACCGAGTTCAATTCTCG
GGCGTCCGGCGCATTGAGCTGGGGTGCCTGCCAGCACCGTACAGTACTGACGATGGTCCACGTCGGAC
GAGCGCTCCACGTCGTCGCCAACGGTATGCATGGCGCTACGATTCTC (SEQ ID NO. 184)

:::::::Rv192T7.seq:::::::
CGGTGCGGACCGGCTCTGCAGTTGGTAGGCTGCAGTTGTGCATCAGGCCATGCCGCGCCGGCTCGTGGCCAC
GCATGTACAGCACCACGCCGCCCCCTCACGGCGACCATGCCAGCGCGTCCAGCTGAGGCCGAAATCGCAGC
GGCGTACCCAAACACATGCCGGTCAAGCACTCCGAATGCAACCCGGACCAGCACGTCGTCACCGTGGCTGGCC
CGCGATCTGCCGCGGACAGCGCAGATGTTCACGTCGTTAGATGCTGGTGTAGCGATGGCGGAAACTCCC
CATGACGAGTCGAATCCGCGCTCGCGACCCGCTCAATGTGCTTCTGCTGCTGCGCCGCAATTGATCAAGTCAG
CAATGGTATCAGGCCAGACCGTGTCACTGGCGAACACCGCAATTGATCGGTGTGCGCCATCGAGCCCTCATCTT
TTGGCTGACGATCTGCAAATGCCCGCGGGTGTGAGCCGGCAT (SEQ ID NO. 185)

Clone Rv193

:::::::Rv193SP6.seq:::::::
ATACTCAAGCTTGGGTGAAAGCCGATCACCGGAAGCCGATGATCACGCCACGTTTCGCGCCGCCGGCATACGGCG
CGTACCGATCTCCGCGTCATACACCCGGGTAATCGCGACGGTGGCGTCCAGCGAAGGTGACGACGCTGAT
TGAATCGAGTCCAGGTCTCAGCGGGTGGCGCAGCAACGGCGAGCTCAACGACGTCATCACGTTGCTGCTTCTAC
GGTACCGACCCGGTGTACCGTNCTGCCCGGTGCGCTGCCGATAAGTTGACCGCCACCACCGGACACCGCTTTG
CACCGGACCCACCCCGGATCCGTTGGCC (SEQ ID NO. 186)

:::::::Rv193T7.seq:::::::
AGCTTGTGGCATCCGCTCCAGTAGCGCCCGCGCTGGCTTCCAGCGCCCGCAGATGCTCCATGAGCGGCCGGTGC
AGTCGGCGCCGGCGTTCACGCCACCGCCAGGAGCTGGCGCCAGCATCTCCGCTTCACGCAATTGCGGATCACAG
AGAGAATATACTGTCATATTGTTGGAGGTGCGCAGGCAATCGTCAATGACGGATTGATGGCATCGAGCTGTG
CTTCGGCGTAGCCCTCCAGCACGTCGGTATCGCTGTTGGCGTCCACGACGACCGCACCACGGCGGGGACACCGCTCG
GGTGGACGNTGTGCGGGGATCAGTCGGCCAGCTCCGCTCGGGATCAGCGGC (SEQ ID NO. 187)

Clone Rv194

:::::::Rv194SP6.seq:::::::
ATACTCAAGCTTGTGCAGCTTCCATGACTGCTCCGAACCTGGGGTGTGCTGCTGTATGACGGCATAACGG
ACATCCTCCCTGAGACCCGGCTGAACCAACGCCAGCTGTCATCACGGGTCACCCGGCAAGGGCGACGGC
ACGCCAAGTTCGCGACCGTTAACCTAGTGTGTTAGCTTCATTCGCTGCGAGAAAACAGCTGGTGGCGTTAGGA
ACTGAATTGAAACTCAACCGATTGTTGGTGCCTGCCAGGTCGGTGTGCTGCGCTGGTGTGTTGCTCCGCTGTGGT
AACNACNACAATGTGACCGGGGAGGTGCAACCAACTGCCAGGCGTGGCGAAGGTGATTGCGGGGGAAAGAAC
TCAAAGCCAGTGGGTGACCGCGAGGCCACGC (SEQ ID NO. 188)

:::::::Rv194T7.seq:::::::
AGCTTGTGGCGAGACGGACACATTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTGAGTCACCAGGCCGA
TCAAGCCTTCGCCGAGCCAATTCCAATCAAGAGGCCAACGCCGTCACCAATCACGCCGGCAACGAGGGATTCCGTCA
TTATCAGCCAAAATAACTGCTCTCGGGTACACCCAAACAGCGCAATATGGCAAAACGGTGGCGTTGCGACGACAT
TAAATGTCACGGTATTGTAGATTAAAAGATACCCACCAACAAGGCAATCAAACGAGAGCGGTTAAATTGACCGTAA

AAGCGTCCGTATCTGTTGACGGTGTCCCCTGGTATCCGACGTTCCATACGCACACCGGCCGGCAGTCTTGTT
GGATGCGTGTGCAGTGGCCTCATCTTGATGATCAAATCGATGTGGCTCAGTCCTCCGGCA

(SEQ ID NO. 189)

Clone Rv195

:::::::Rv195SP6.seq:::::::

ATACTCAAGCTTCGGCTCAGGCGCGCTGCTGGTAAAGTCGCTGACCGGTGCAGGTTCGACAATGTGGGCCGGTTC
GGCGCGTACGTGCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTC
TTGAGCATGAGTCGGCGACCGCTCATGGTCACACCCACGACGGAAAGACGAGATCGCCGTCAAGCATGTGTGCC
GCGGATTATCAGGACTGACCTCTGGCTGACCGGCATGTTGGTCGGATGCCCTGGCAGCCGGCGTGGTGTGG
TCCGCTGGATAGCGAGGTAGCGAAATTNCNTGGCAGCTCAAAGGGTCTGCCGGTGCCGGTCTTGCACAAACNA
AGGCNCAGGTTA (SEQ ID NO. 190)

:::::::Rv195T7.seq:::::::

TGATCGCGCATCACCTGCTCATAAACTGGAAGCAGCGCAGCGCTCTTTCGGCCAACATGAGCCAGCCTCTCG
TCGGCGGTGGGTGCAGGTGCTCGGGCAGCTCGGCCGAGCGCGCTGACCCCTGAAACCGACTTCCATATCCCGCG
ACGAACGACGCCAGTCCGCTACGTAACCCCTCCGCACTGTCATGGACAACAGCGCGTCTCCACCGACCGGGCCCG
GGTGTGGGGTGTTCGGCGACCGGCAGCCAGGTGGTCCACACTGCCGACGGGCCGCGAGCCGTTACCGACCGAC
CGCCGAGCAAGTCCGCCGATCGCATACTCCAACCGTTGCGGTACTGCAGGTTAGCTGGGTACTCCTCGTCGCGC
TCGGCGAGGTCTGCTCCAGCACGTCGACAGGCA (SEQ ID NO. 191)

Clone Rv196

:::::::Rv196SP6.seq:::::::

CAAAGCGCGAAGTGCCTCGCCAGGCCACGACGTGCTGCCGATTGCCGGCGAAATCAATTCCAGGCAGCTCC
CGGACAATGCCGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTACCCCGGTGCCGGGTGCGTGGTCACCTGCCGA
TCGCACAGGTGGCCCACAACCGCCGCTTGATGCCGGTGGCAAGCCGGCAGTTGCCAAACCCAGCGTGTACAGG
CTCGGCTCGCAGTTCCGGAAAGAAGTGGCTCCGCTGATCACCTACCATCCGCCAGGATCTGCGTGTCTCACCACG
CCCGCAAGGAGGTTGTTGTTGCGTATCGACCGN (SEQ ID NO. 192)

:::::::Rv196T7.seq:::::::

CCGGAAGCCGCATGATCAGCAAGTTCGCGCCCGGACATGGCGGTACCGATCTCCGCTCATACACCCCGCG
GGTAATCGCCGACGGTGGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTTCCAGGTCCAGCGGGTGGC
GCAGCAACGGCGCGAGCTCAACGACGTCAATCACGTTGTCGTTCTACGGTCACCGACCCGGTGCACGTNGTCGCC
GGTGCCTCGCCGAAANNTGACCCGCCACCGCGAAACCGTCTGCACNCCGAAGCCACCCCGATCCGTTGT
TGGGCCAGGTTATTGGGT (SEQ ID NO. 193)

Clone Rv19

:::::::Rv19SP6.seq:::::::

CCGGAACCGCCGACGGCACGGTATAACGCCCTCGCATATGGTCGACAACCCAGGGTGGACTTCTGGCTTCTAGC
GTTCGCGCNGTCGCACAAACAGCCGGTCGAACCGACACTCGTTGATGTCCTAGCTACGTTGCGTACGCACC
CAATCGAGTCTAGCGCGGGTAGNTCAGCCCCGATCTCCANGCTCGCCGAGCCAGGCG (SEQ ID NO. 194)

:::::::Rv19T7.seq:::::::

CTGGTTATGTCGGTTGAAGTTCCATCACCGATGTTGGCGGGAGCAGTGCAGGTGATCTCAACTACCACATCCGG
CCGTGGCGGTGCGCGCCCCGGGGTGGCGGAACCTGACGAGGGGGTGGAGAAATCGCCAGCACCCCGCTGAAC
CGCGACCACCCGCTGTTGGAGATGTTACTCGTTGAGGGGTTGCCAACACCAGGATCGCGGTGGTTGCC

(SEQ ID NO. 195)

Clone Rv1

:::::::Rv1SP6D2.seq:::::::

CCGAGCAGTTGGGAATCGCTCTGCACCAAACCAATATTCTGCGCAGCTCGCGACGAGCTGGACCGATTAGGCATA
CGCCTCCGNCNTGGACGACACGGGGCACTCGATGACCCCGACGCCACGCTCGCAGGATATTGTTGCCGGACCCCTC
TCTAG (SEQ ID NO. 196)

:::::::Rv1T7.seq:::::::

TATATAATACTCAAGCTGCCGACGCCAACGCTCGCGCATGTTGTTAGCCGACCCGGCTTACATGGCACCGGTG
CCCCACACGTAGCCTGTGACGTCTGCACCGCAACTCTTACATAGAAATGTGGATTGCCGGATTGGGGATGTCGGC
ATCGCTCAATCTGTTAGTCCGCGTGTCCCGAGGGCATGTGGATGGGGGAAGGATCCGTGGCTCCGGATCACC
ATGGGG (SEQ ID NO. 197)

Clone Rv201

:::::::Rv201SP6.seq:::::::

ATACTCAAGCTTGCCTGAAGTTCCGATGGTCGCCGCCGAGCCAAACGAAATCGCTAGCGTGGCCGTGTTCTGGCT
 TCGGATCTATCCTCGTACATGACCGGCACCGTGTGGACGTACTGGCGGCCGTTATATGACACCGAGATCATTGC
 CACGGTACGGAAATTCTGTCAGAAGGAAATCTTCCCAATGACCCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGA
 AATCGTCAATCGGCTGGGTATTGGCTTGCCTGGTGCCTGGCTGAGGGTTCTACACCACCGAGTTCAATTCTCG
 GGCGTGCCTGGCGCATTGAACGGCGTGCCTG (SEQ ID NO. 198)

:::::::Rv201T7.seq:::::::

GCACCGCGTCTCGCAGTTGGTAGGCCGAGTTGTGCATCAGGCCATGCCGCCCTCGTGGCCACGCCATGTAC
 AGCACCACGCCGCCCTCACGGGCACCATGCCAGCGCCGCTCCAGCTGAGGCCGCAATCGCAGCGCGTGC
 CCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGGACCGCACGCTTCACCGTGGCGTGGCCGATC
 TCGCCGCGGACCAACGCGACATGTTAACGTCCTCGTAGATGCTGGGTAGCCGATGGCGGAACTCCCCANGACAA
 GTCGAATCGCGCCTCGGCAACCGCTCAATGTCCTCTCGTGTGGCCGATTC (SEQ ID NO. 199)

Clone Rv204

:::::::Rv204SP6.seq:::::::

TGGTCCTGTGCGCATACCAATACAACGCGCCGGCACCTGACGCCGGCCGAAACCAATCGTGGCCATGCCATC
 TTCTGCTACCCGGTCAACGACGACCTCTCCTGGCGACGTAGTGCCTGGCCACCCGCGCTGCGTCCCACGATC
 CCGGTCAAC (SEQ ID NO. 200)

Clone Rv205

:::::::Rv205SP6.seq:::::::

GGCGTGTGGCACCGGGGCACTCCGACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCC
 GACTTTCCGCGGTACCCGCTCAACTTGTGTCACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCA
 ACTAC TTCATCCTGACGCCGGAACAAATTGACCGAGCGGTCCGCTGACCAATACGGTCGGTCCACGATGACCCAGTACTAC
 ATCATTGCAACGGAGAACCTGCCGTGCTAAAGCCACTGGCGATCGGTGCCATGTGGGGAACCAACTGGCGAACCT
 GGTCACCAAACCTGAAGGTATTGTTACCTGGCTACGGGACCCGGCTATGTTATTGACCTCCCCGCCAA
 (SEQ ID NO. 201)

:::::::Rv205T7.seq:::::::

CGTCCGTGNCCTCAANCGGTGNNGCGAAGCGGCTGGTTACGACTCCTGTTGATGGACACTTCTACCAACT
 GCCCAGTGTGGGACGCCGACCGCCGATGCTGGAGGCCTACACGCCCTGGTGCCTGCCACGGCAGCGANCG
 GCTGCAACTGGCGCGTGTGACCGGCAATACCTACCGCAGCCGACCCGCTGGCAAGGATCATCACCACGCTCGA
 CGTGGTTAGGCCGGTCAAGCGATCCTCGGATTGGAGCCGGTGGTTGAGCTGGAAACACCAGCTGGCTTC
 AGTTCGGACTTCAAGTGCACGGGTCACCCGGCTGAAGAGGGCGTACAGATCCTCAGGCAATGGTCAAGGGTGAGC
 GCCAACGTTTCGGCGATTGGTACACCGACGATC (SEQ ID NO. 202)

Clone Rv207

:::::::Rv207SP6.seq:::::::

CCGCTTCCGTGAAACGAGGCAANNGCGAGCGANGGCAGGAAGCAAAGAAGAAACTGTTCTGTCAGATAGCTTACG
 CTCAGCGCAAGAAGAAATATCCACCGTGGAAAAACTCCAGGTAGAGGTACACCGCCGATAGCCAATTCA
 GAGAGTAATAAACTGTGATAATCAACCCCATCAATGATGACGAACATATCCCCGATATCAGGTACATGAC
 GAAATCAACTGTGACAAACTGCCCTCAATTGGCTCCTTAAAGGATACAGTTCAAAAGTATGAGAAAATCC
 AGGCTGAAGGAAACAGCAAAACTGTGACAATTACCCCTCAGTAGGTGAGACAAATGTGACGAACCNCCCTCAA
 ATCT GTGACAGATAACCTCAGACTATCCTGCTCATGGAAGTGTGATATCGCGAAGGAAATACGATNTGAGTC
 GGTGCCCTTCTTCTCAATGTATGAGAGCG (SEQ ID NO. 203)

Clone Rv209

:::::::Rv209SP6.seq:::::::

TGACACCCAACAGAGGGCACTTAAGATGGCAATGCCGCCCTACCTGCACGTTTCCGATGTCAGAGGATGCCGAG
 GGAGAACAAATCGGAGCACGCCGCTGACNTTGCTACCGCTTGGCGCCGTGACATGGTGGTGGTGC
 AGGCCGANTCAGGCCGAAGCATATAGCGCGCCGACCGCATTGCTCGACCGCAAGCGCAGCTCAGGCCGAGC
 CGGTGGAGCTACTGCTGCCCATCACGCC (SEQ ID NO. 204)

:::::::Rv209T7.seq:::::::

ACGGGCGACGCTGAGGTGGGCCGCGCTATTCTCATGCTGCTCCACGTCAGCGACCGACTGCCAGACGGCC
 CAACTAGCCACCTGGGTGAGAACACCCAGGACTGCGTGGCGCCCTCGGATCTGGCTACACGCTGGCGTGGCG
 CGCGCAGCGCCGGTGCACCGCAGCGTGGTGCCTGACCGCAAGCGCAGCTCAGGCCGAGC

GGTACCCCTATGACGCGCGGTGGACACTGTGATCTAAGACCGGTGGGCTTCTCCGGGCAAGGGCTCAGT
GGCGCGATGGCACCCATTGCTGCCAGCGAACCACTGTTCGCGGCCACCATCG (SEQ ID NO. 205)

Clone Rv20

:::::::Rv20SP6.seq:::::::
ATACTCAAGCTCGCAGATCCGGATGGCACTCACGCTGGACAAGACCTCACAAAATCTGAAATCCTGACCCGATAC
TTGAACCTGGCTCGTCCGGCAATAACTCGTCCGGCTGCAGGACGCGGCAAACGTAACCTCGGCATCAACGCGTCC
GACCTGAATTGGCAGCAAGCGCGTGTGGCCGGATGGTCAATCGACCAAGCACGCTCAACCCGTACACCAACCC
GACGGCGCGTGGCCCGGGAACGTGGTCTCGACACCATGATCNAAAACTCCCCGGGAGGCGGAGGCCTGCGTG
CCGCCAGGGCGAACCGCTGGGGTCTGCCGAGCCCAATGATTGCCGCGCTGCATCGCAGGGCGAACCGCCA
TTCTCTGCGAATACGTCCAGGAGTACTGTCTGGGGC (SEQ ID NO. 206)

:::::::Rv20T7.seq:::::::

AGCTTATGTGGCGCCACCTACCTTATCTAGCTAGCTAACTAAATCCAGTGCCGACAGTGCGGGCTGGCCACCCA
GCATGAGGTTATGACCACGGCATATGCCAGCGCGTGGCGGGATGCCGACGCTGACCGAGTTGCCGCTAACACAC
CAGCCATGCGGTGTTGCTGGGAACGAATTCTTGGAAATCAATACGATCCCAGTCCGCTCAATGAGGCCGACTATGC
GCGGATGTGGATTCAAGGCGGCCACCACGATGAGTATCTATGAGGGCACCTCCGATGCCGCTGGCGTNGCAGCGCA
AACACACCGGCTCCGGTACTGTTAACGGCGGTGCTGGCGTTGCCAGCGCCTGCCGGCATCTC (SEQ ID NO. 207)

Clone Rv214

:::::::Rv214SP6.seq:::::::

ATACTCAAGCTGCCACCATGCCAGCAAGGTGCACTCAGCGATGACGAATTGTTCTTCGCGGTGTTGCTGCTG
GTTGCGGGCTATGAGAGCACTGCTCATATGATTAGCACNTTGTGACTGCGTGGCCACTATCCAGATCAGCTGACA
CTCCTTGCGCAGCAACCAGACCTGATCCCAGTCCGCGATCGAGGAGCACCTCCGTTATATCGCAATCCAAAACATCT
GCCGACAACGCGCGTCACTATTGCGTGGTCAAGCGGTATCCCAGGA (SEQ ID NO. 208)

:::::::Rv214T7.seq:::::::

CCGGGGTAGAACGATGCGATCTGGGCATGTCGACATCGGTGGTACAGGTAACCGCGCCGTGCGCGGTCTCGGAG
ATCAGAACGTGGTGCAGTGTGACACCGCGGGCTTCAGCCAGTCGCGATAATCGGCGAAGTCGGCGCTGCCGCCCCA
ACTAGCGCAGCTCGCACCTAGCACACCGATGGCGAAGGCCATGTTCCGGCACGCCGCCGGTGCATCATCAAC
TC (SEQ ID NO. 209)

Clone Rv215

:::::::Rv215SP6.seq:::::::

ATACTCAAGCTGGCGCAACGCCACTACCGGGCTCACCAGGTCTGTGCCGCCACCGCCGGGCCAAAGCACCATC
AGGTGCTAGTTGCTGGACGTTGACACCGTAAGCGAACACAATGCCGCCCATGCTGTGCCGAGCACGATGCG
TTGACCCGGGATATCCCGGGTGGCGATCCCAACGAGGGTGTGCAAGTCAGCGGTGATCTGAGATGTCTCACTA
TCATCCGTTGGCACCCGAGCGGGCATGCCGCCGGGGTCAAC (SEQ ID NO. 210)

:::::::Rv215T7.seq:::::::

GTCGACGGCATCAAGGTCGCAAGTGTGTTCATCTCACCCAGGAAGGCGTGAAGTGGCTGATACCGTGGCTTGAG
GATTGGTGCAGGTCGCCAGTTAATCCGCCGTGTCCTGGATGAGCGCGACGGTAACCCGGAAATTGCTGTGCTG
TGGCTGTGCTGTTGATGAGCGTCTAAGTGGTGTGTAACCGTTGACGAGGCCGCGCTCGCTGCAAACATTGAA
GCCCGCACGTCGGTTGATTTACACAACGAGGGCGCTCCCGATCTGGCGGCCAACGAGGTGCNCACTATCCA
TTCGAGGTGAACGGACTCCTGATGCTCATGCCGGTGCAGGTTGTC (SEQ ID NO. 211)

Clone Rv217

:::::::Rv217SP6.seq:::::::

ATACTCAAGCTCGTTCGATGAAGTAGTCGTCGTCAGCGCCGCTTCTGAGCTCTTGGCGATGCCAGCAAGGA
GTCATCGCCGCCAGCTGGCCAGGATCTTGTGCGCTGTTCTTGACGATGCCGCCGCGGATCGTAGTTCTGTA
GACACGATGACCGAACCCATCAATTGACCCGCCCTCGCGGTTCTGACCTTGGCTTACAAACTCGCTGACGTCG
CGCCGCTGTCGCGAATGCCCTC (SEQ ID NO. 212)

:::::::Rv217T7.seq:::::::

NGTCAAGCGAGCATGCGCGAGGNAACGACGAACCAACAAGCCATGGTGGTGGCGCCGTCGAGAGGTGCGCGGTG
CCACAAAGGGAGATGCCCTGAGCGTCGCTGACCGCCGCTCGAGTTGGGTATAACGAAGTAGCTGATGCCGATC
ATGTCGACGTTCCGTCGATCAGCGTGCAGCGGGCACCCACTCGACGAGGTCTCGGTGCCGCCAGGGCACC
AGCAGTGACGATTCCAGGCGCCGTCGGG (SEQ ID NO. 213)

Clone Rv218

:::::::Rv218SP6.seq:::::::
 CGATAATCGCTTCCGGTAAGTGCAGCAGCTTACGACGGCAGTCCCCTCGGCAATTCTATGACACCAGATACTCTT
 CGACCGAACGCCGGTGTCTGTTGACCAAGTCAGTAGAAAAGAAGGGATGAGATCTCCCGTGCCTCAGTAAGCAGC
 TCCTGGTCGCGTTCATACCTGACCATAACCGAGAGGTCTTCTCAACACTATCACCCGGAGCACTTCTAGAGTAAAC
 TTCCCATCCGACCACATAGGCTAAGGTAATGGCATTACCGAGGCCATTACTCCTACGCCGCAATTAAACGAAT
 CCACCATCGGGCCGCTGGTGTNC (SEQ ID NO. 214)

Clone Rv219

:::::::Rv219SP6.seq:::::::
 NAATACTCAAGCTTCTCGTATTACCAACCGTGTAAATTGGGATGGGAAAAAGGCGAATCACCGCGTGGCCACAAA
 CGCCGGGAGGGACAATCTGGCGGCTAGGGCTCTCGCGGAAGGCCAACGTACGGCGTTCAACACCGTCGCGTC
 GCCCTCGAACCGCGAACATTGGGATGGCAGCAACCTGGTATCACCTGGCCGGCAATGATCTGAGCGTCGCCGC
 GGGTAGTGNCCGCCGGCGCTAC (SEQ ID NO. 215)

:::::::Rv219T7.seq:::::::
 CCAACTAGAGCAGTCGGACATACGGAGTCAACTACCCGGCAACGGTGTATTCTGGCCGCCGCTGACGGCGCAACG
 ACGCCAGCGAACACATTCAAGCAGATGCCAGCGCGTGCCTGGCCACGATGTTGGTGTCTGGCGGCTACTCCAGGGT
 CGGGCGTGTGATGACATCGTCACCGCCGACCACTGCCGGTCTGGGTTCACGCAGCCGTTGCCGCCGAGCGGAGC
 ATCACATGCCGCGATGCCCTGTTGGGAAATCCCTGGGGCCGCTGGCGGCTGATGATGCCCTGACCCCTCAA
 TTCGGGCTCAAGA (SEQ ID NO. 216)

Clone Rv21

:::::::Rv21SP6.seq:::::::
 ATACTCAAGCTGCTGCAGCTTCTGTGACTGCTCCCGAAACCTGGGGTGTGCCTGCTGTATGCACGGCATAACGG
 ACATCCTCCCTGAGACCCGCGGTCAACCCAGCCACGTGTCATCATCAGGGTCAACCCCGCCAAGGGCGACGGC
 ACGCCAAGTTGCCGACCGTTAACCTAGTGTGTTAGCTCATTGCTGCGAGCAAAACAGCTGGTGGCGCTGGTAGGA
 ACTGAATTGAAACTCAACCGATTGGTGCCTGGCTAAGTGTCCCTGGCTGGCGCTGGTGT (SEQ ID NO. 217)

:::::::Rv21T7.seq:::::::
 AGCTTGCAGCGCGTGGCGATCGCGTCAAGGCGCGCTTCAGAGCACAACGAGCGAAGACAGCTGGCGACGGAGCC
 TTTATCGACATCCGTTGGCTGGCTGACCGGGCGAAGAACTGCTGACCGTTGGTGTGACGGTGGCGTGGCGA
 GCCGAGCGCCGTCAGATGTACGACCGGGTGGTGGATGTGCCGCGCTGGTGAAGTTTCACGACCTGACCATCGAAGAT
 CCGCCGCATCCGAGCTGGCGGATGCGCC (SEQ ID NO. 218)

Clone Rv220

:::::::Rv220SP6.seq:::::::
 AATACTCAAGCTTGCACGACCAGGACGTCGAGTGGCGCTTGCAGTGACTTGGCACCTCAAAGGCCACCGGTACCC
 CGCCCGCGGCAAGCCAAGGACNACNACGGCTTGCGGATAGCTGCCAGGCAGTGCCTCCAGCGT
 CGCCACGATCGTCAAAGAGGCTTCATCGCGAGTGTGCGCATCTCATGGCTCAAATATGAAATTAGGTCCCTGG
 CCGACTGACGACAGTCCCTCAGCGACCGGATTGCGCATCCCGCTTGTACGCTGCTCCGCAAATCCGGCTTGC
 CGCGGAAGCGAACTCGGCGCGTACGGTGGCTACTTCGGCGTGC (SEQ ID NO. 219)

:::::::Rv220T7.seq:::::::
 GGTTGGTGCCTCACCTCGCGCGCGCGATATGCCCTGGCTTGCCTGCTGCTCATTTGATATCAAATCTATGGGT
 CGTGGTTACTCAGCGGGCGAAGCTGGCCCTCCCACGGGTAGGGCCCTATTGACGGTGTGCCCCATCGACCGAGCG
 TACCGCGATGATCTGGCGCAGCGTCAGCTGCTGGCGTGGCTTGTGCGGCTCCGCCAACCTTCGCCACACCGGGCT
 CTTGATCCCAGGTGACTTGGCGACCTTGGTCTTGTGCGGCTCCGCCAACCTTCGCCACACCGGGCTTAAGCA
 GCAGCTTGGCGCGGGCGGTCTCAGCGTGAAGTGAAGCTACGGCTTCTACAAACGGTGTACGCTGCTCCGCAAATCC
 CGTTGCCGCGTGGTCTCCGTCGCGCGTGTACGCCCTGAGAACTCCATGATGTTGACCCGTGCTGACCGAACGC
 GGGGCCACTGGCGGGGC (SEQ ID NO. 220)

Clone Rv221

:::::::Rv221SP6.seq:::::::
 ATACTCAAGCTTGCACCCGCAAGGCCGGTGCCTCCCTCGTTCCGCTGCCCGGTCTGCTGATCGGTTGGGGT
 CGCCCGCGTAGGCCAATTGCCGGCTCCCTCCTCGGGCTTCCACAACCCGATCGTCGCCGGCTAGGTTCAAGGCC
 ATGCCGGTAAACCCAGGACGCCAGTGTGATCGGCTATGGACAGGTCAACCACCGAGGCGACATCGACGCCAAAAT

CAGTCCATCGAACCCGTCGACCTGATGGCCNCGGGCGAAAGCCGCCGAGTCACCGTGCCTCGAAGCGGTGGAT
TCCATCCGTGTGGTGCACATGCTGTCGGCGCATTACCGAATTCCCGGGCTCTCCCTCGG (SEQ ID NO. 221)

:::::::::::Rv221T7.seq:::::::::::
NCCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCTTTGGCCGAAACATGAGCCAGCCTCTCGTCGGCGGTGG
TGCAGGTGCTCGGGCAGCTCGGCCGACAGCCGCTGACCCCTGAAACCCAGCTTCCATATCCCGCAGAACGACGCC
AGTCCGCTACGTAACCCCTCCGCAGCTGTCATGGACAACAGCGCTTCCACCGACCGGGGGGGGTGTTGGGTG
TTCGGCAACGGCAACCAAGTTGGTCCACACTGCCGACGGCGCCGAAATCCGTTACCGAACCGAGGCCCNAAACA
ATTCCGCCCGATCCCATAT (SEQ ID NO. 222)

Clone Rv222

:::::::::::Rv222SP6.seq:::::::::::
ATACTCAAGCTTGTGGGATCAATCTCGAGGGCATCCACGCACGAAAAGTAAACTCTATCAAGCTTTTGACGACACC
CACGGACGCCCATATATGTTGGGTGGGCAAGAACGGTCCCTACCTGGAAACGTTGGTGGCCGGGACACCGGTGAG
CCCACGCCGAGCGGGCCAACCTCAGCGACTCGATTACCCGGACGAACGACTCTACAGGTGGCGAAGAGCTCTTT
GCCACACCGCAACAGGGACGGACTTGGGCTTGGACCCAGAAACCGGCCACGAAATCTTGCCAGGGGAAGGCCGGTT
TGGGCTTATGTTACCTATATCTGCCGGAACCTGGGCTGATGCCGGCGCCGCTAGGGAN (SEQ ID NO. 223)

:::::::::::Rv222T7.seq:::::::::::
AGCAGCTAGCCCGCCTCGCCCGCTGGTCGGTGCATGCTCGCAGCCGGATGCACCAACGTGGTCGACGGGACCG
CCGTGGCTGCCGACAAATCCGGACCCTGCATCAGGATCCGATACCGGTTCAAGCGCTGAAAGGGCTCTCGACT
TGAGCCAGATCAATGCCGCGCTGGGTGCGACATCGATGAAGGTGTTCAACGCCAAGGCAATGTGGACTGGAGCA
AGAGCGTGGCCGACAAGAATTGCTGGCTATCGACGGTCCAGCACAGGAAAAGGTCTATGCCGCACCGGGTGGACC
GCTATGCCGCGCCAACGGCTGGATGACAGCATCGATGACTCCAAGAACGCGACCACTAGCCATTCAAGCGGTGTC
GGCTCCGACCGCACATGATGCCGAAGAATTCTACAGCTCCCG (SEQ ID NO. 224)

Clone Rv223

:::::::::::Rv223IS1081N1400.seq:::::::::::
CGCGACTGGCTCCCCGGNCGGCTGTCGGTCCGGCAGATAGAGACCGGGATGTCGCCGACGACGGGAGCCGGGTTG
CGTGGGACGGGGCGGGGTCGGGAGCCAAAGCAACGGGCTAGTCCCCGAACTCTACGGAGCCGTCACCTACGCCCTAC
GTAATAGTAGCTATCAATAACAGTTGACATACGCACAGATCTGTGAGATCAATATTGCTGACGCATGTCAGACAGG
CGTCAAGACAGGTGTCATAATTGCTCCGCTGGTACGGTAACCGGTGTCGGGTGACGCCTAAGGAAGGAG
TGTGGTGGTACGCTGAGAGTGGTTCTGAGGGTTGGCGGCCAGTGCAGGTTGGAGGCGTTACCCGACCG
TGGCGCCGACACGCTGGCGCCGGCGATACGGCGTGGTGGCGCCGCGGATCCGGTGTGAGAAGGAG
ATGCCGGTGGGTTAGCGCTTAAGTAGCCAGCATGCCGATGCCGGAAAGGTCAAGAACGACTGGGT (SEQ ID NO. 225)

:::::::::::Rv223SP6.seq:::::::::::
ATACTCAAGCTTATTGAACCGCGGGTCGAGGAAAGTGGACCTCATAACGACTCGGGTCCAGCGACCGGCCAACAC
GAACGGCCGGACGCTGGGCCAGGGTCGCGGCCCTCCCCCTACAAACAGGATCCGTTGCCTGCAGACAGGCTCCGG
TGCAGCTGGGCGCCGTGCTCGCCAGCGTCCGGTCCGGTCGCCGGGAGCCTGTTCTCCATACTCGCCCC
CTAATCTCGAGGGCAGCCGTACCCGAGGCAACCTCCAAAATGCAATCCGCAAATGCAATGCGTCAGCTATT
CTCACACCGACCCGCTAGTGCAGGATCAGAAATCCGTTGGCGGAAAGTCCAGGCCAAATTGTTCTCCGCTCCGCAT
CATGCTTGTAAATGTTGGAAATTCTCCATATGCCCTGATCGCTTACAGGGTCCAGGCCAAACCGGGCAGGA
CTGGGTGGCGTTGATGTTGGAACTCTCCACTACTAGGTATTACCGGC (SEQ ID NO. 226)

:::::::::::Rv223T7.seq:::::::::::
GTCTCGATCATGGCAAAGAGCTCGACGAAGCCGTAGAGGGCTTCGGACCCGCCGCTCGATGCCGGCCGTATACC
TTCCCTCGCCGCCGACGCCCTGGTGCCTCAAGGTGCGCAGGGCAGGCCGCTGTCGGGTGACACACCTGATGCCACC
GGCGTCAACGCCGAGGGCTACCGAGAGATCCTGGGATCCAGGTACCTCCGCCAGGGACGGGGCCGGCTGGCTGGCG
TTCTCCGCGACCTGGTCGCCCGCAGGGCTGTCGGGGGTCGCCGCTGGTCAAGGCCGACGCCAACGCCGGCTGGTGGCC
GCGATCGGCCACCCCTGCCCGCAGGGCTGGCAGCGCTGCAGAACCCACTACGCAGCCAATCTGATGGCAGCCACC
CCGAAGCCCTCCGGCGTGGGTGCGCACCCCTGCTGCACTCCATCTACGACCGACGCCGACGCCGAATCAGTTGGGCC
AATATGATCGGGTTCTCGAC (SEQ ID NO. 227)

Clone Rv224

:::::::::::Rv224SP6.seq:::::::::::
ATACTCAAGCTTGTCAAGTTCATGGGCCAGCACCAACAAAGAGCATCGGGACATACGGAGTCAACTACCCGCCA
ACGGTGATTCTGGCGCCGCTGACGGCGCGAACGACGCCAGCGACCAATTCAAGCAAATGCCAGCGCTGCCGGG

CCACGAGGTTGGTGCCTGGCGGCTACTCCCAGGGTGCAGGGTGTATCAAGATCTTCACCGCCGACCACTGCCCGGCC
TCGGGTTACGCATCCGTTGGCCCGCC (SEQ ID NO. 228)

:::::::Rv224T7.seq:::::::
GCCCGTGTAAATTGGGATGGCAAAAGCGAACGCCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCT
AGGGCTCTCGCGGAAGGCCGAACTACGGCTTCAACACGTCGCGTCGCCCTCCGACCGGAACATCGGGGAT
GGCAGCAACCTGGTAGCACCTGGCGGCGATGATCTGCAGCGTCGCCGGTAGTCTCCGCCGGCGC
(SEQ ID NO. 229)

Clone Rv225

:::::::Rv225SP6.seq:::::::
ATACTCAAGCTTCTTGACCGAACCGCCTCCACCGCACCGTGAGATTGGTGGCGCATTGTCGTGGTAGCTGCTG
TTGGCGCGTGCCTGATGTGCGGGCCAGCCTTGTGCGGGGGCGCTTCAACACGTCGCGTCGCCCTCCGACCG
CCCAGCTGACCGCGAATTACGGCGCCGCAACGCCGCCGGAGGGCGTACGCAATCGTTATCCTTCAGGTTCC
CAAATCCTCCGCTTACTGGTCTCATCGG (SEQ ID NO. 230)

:::::::Rv225T7.seq:::::::
GGCAGCGCGACAACCGAACGTCCGACGGTGCTCAATCACGGTGACGGTGTCATCAGAATGGCGGGGTTCGT
TGTGCGGTGAGCGTTCGGCGAGGAGGTAGTGTCTACCCCTTGCAGGGCTGGTAGTGCAGACTGAAAGGGATTTCAT
TGGGAACCCACGGCTGCGTATCGCAGGGCTCGGTGACGTCGCTTCCTCNAGCTAGGAAGTCGGCGAGAATCTCG
GTGGATGTTATTGGTCCGCTAC (SEQ ID NO. 231)

Clone Rv226

:::::::Rv226SP6.seq:::::::
ATACTCAAGCTTCTCGGCTTCTGTAGCCTGAGAAGAAACCCAAAGTTAACCGCTGCTTACCTTCTCCAGC
GCCGGGTTATTTCTCGCTTCCGGCTGTCATCATTAAACTGTGCAATGGCGATAGCCTTCGTCAATTICATGACCA
CGTTTATGCACTGGTTAAGTGTTCATGAGTTCAATTCTGAACATCCTTATTGTTTGC
(SEQ ID NO. 232)

Clone Rv227

:::::::Rv227SP6.seq:::::::
ATACTCAAGCTTGGTGACCGCACCGCATACTGGCGAGGCATCTGGCTGGCGTGGTCGCCGCTCCGAAGCC
GTCGAACACCATGCCAGCGCGCTCCACATCAACGACCATTGCGCAGCTGCGCGCATAGCGGTTGCGAT
GAGCGCCCCACCGAATGCCGCCGCTGCCGGCGTACATCGATTGACCATCGCGCGCGCGTGGCGAGGGC
GAACGAGGCGGTGCCAACCGCAACTGTTGGTCAGCTCCCTCATGGGGTTGATTCTTGCCGTCCGGACGGGCC
GCGTCATGCGCTGGTCG (SEQ ID NO. 233)

:::::::Rv227T7.seq:::::::
CCGTTGCGCAGCGTGAGCCGATAGTTGACATCCGGCTCGGTGAAGGTGAAATCGATGGCCAGGTGAGGTCCCATGCG
CGTGGGCCATTGATGCTGATGCCAGGACGTAAAGATTGGTCCGGCGTCAAGCTGGCGAAAAACGTTGGCGCCGG
ACTTGCCCGGAGCTGCCGGGTTCCCGTGCAGCTCGCCGGCCCGTCAAGAAAGAAATTGCGCAGGTGCGCACAC
TCCGCGCCGTAGGCCAGCTGCTCCAGGGTGTGCGCATAGAGCCCGCGGGCCGAGCGTGTGCGTGTGGCGAACACC
GCATGGTCGAGAAGCGTTGCCGCCAACGGAAATCACCTGCGTCGAAAGCTCGCGGGCAGCTCCAGCAGCGTC
GATGCCACCCAACCGCGT (SEQ ID NO. 234)

Clone Rv228

:::::::Rv228SP6.seq:::::::
ATACTCAAGCTTGGATGTTACCCCTGACAGCGTAACTATGTCNAAACACACGGCACCGAACGGTGTGGGGGAC
CCCACATCGAGTTCGAGTCGCTGGCGGCCACTTATGGCTGGTAAAGGCCAGGGCGAGAGGCCGTGCGCATGGGTGCG
GTCAAAACCAACATCGGCCACCTGGAGGCCGGCGCCGGTGTGGCTGGATTCAAGGGCGTGTGGCGTGCACAGT
GGGCACATTCCCCGCAACTTGCACTTCACCCGGTGGAACCCGGCATCAACACGTCGCGACGCCGTGTTGCG
ACCGAAAGCGCCCCGTGGCGGCCGGCTGCCGGTCCACGCAAGGGCTGCGGTGTCATGTTGCGCTCAGCGGGACCAA
(SEQ ID NO. 235)

:::::::Rv228T7.seq:::::::
CCGTAACCAGATCAGCTCGTCGACCTCACTGCCGGGGTGAATTCCCCACCGGTGCTGCGCGTGCCTGCCAGTAGTGC
CCTCTTGACGCCCTGAAAAGGGAGTCGGTGGTAGGTACCGTCAGGAGCGCCTACCCAGGTGGCGGGTGC
CGGCTCCTCGAGTATCTCCCGCACCGCCCCACCGGTGCGGTCTCGCCCGGATCCACTTGCCTTGGCGAGCGAC
AGTCGTCGTAACGGGGCGGTGAATGACAGCGATCTCGACCCGGCTTCCGAATCGGCACTGCCGGTGCAGAAC
CCGACCGCGCGTACACAATCCGGCCGCCAGCGCCGGGGCGAGCAGCTGGATCAGCACCTCAACTCTCG
CAGGTCAATTGGCCAAGCTGCTCGGGTGTGGTC (SEQ ID NO. 236)

Clone Rv229

:::::::::::Rv229SP6.seq::::::::::

ATACTCAAGCTTGTGCCGCCGAAACCGAGCGTGAGCACGCCACCCACCACGCCGGTGGGCCGGGCCGG
 GCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCAGACACCACCGCTGCCCTACGCTGAGCCATACCGGGCG
 GAGCTACATCGGCTCGGCCGCCCAGTGTTCGGCCCTCTTCGAGGTCGAGGTCTATACCGATTGCGCATCCGCAGC
 CGCACCCCTGGCTCGTACCGTGCCCTACCTCTGCTTGTCCGGCGGGCCA (SEQ ID NO. 237)

:::::::::::Rv229T7.seq::::::::::

TCGGTACGGCCCGGGTACGCTTCGGTGCAGTGTGCGAGTGATAGATGACGACCAGGACCTCGTGGCATCTTCCATA
 GCCGCCACACCTTCAGTGCTCACCGAATCCAACCGTAGAAGGTCGGCGAGCGCTGCCATTGGTCATCGGGATA
 TGCCGCTCGGACGGTCAGAGCCCTCGGTCCGGCCAGCACTCCGCAGGCTTCGTCGGGTGGTCGACGCGCATGG
 GCCACCATCCATCCACCAGGTCTGCCGAATACCCGC (SEQ ID NO. 238)

Clone Rv22

:::::::::::Rv22SP6.seq::::::::::

GGACACATTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTGAGTCACCAGGCCATCAAGCCTCGGCCAG
 CCAAATTCCAATCAAGAGGCCAACGCCGTACCAATCAGGCCGGCAACGAGGGATCCGTATTATCAGCCAAAATAA
 CTGCTCTCGGTTACACCCAAACAGCGCAATATGGCAAAACGGTCGCCGTGACGACATTAATGTCACGGTATT
 GTAAATTAAAAGATAACCCACCAACAAGGCAATCAAACGTAGAGCGGTTAAATTGACCGTAAAGCGTCCGTATCTG
 TTTGACGGTGTCCCGTTGGNTCCGACGTTCCATACGCACACCAGGCCAGTCTTGTGGATGCGTGTGAGT
 GGCCATCTTGATGATCA (SEQ ID NO. 239)

:::::::::::Rv22T7.seq::::::::::

GCCTGGCCCAGGTGAAGGCCGACCTCGACGCCAAGCCGCTGATCCGCCACATGAGTCGGTGGACTGGGACTTGAAGT
 CGCTGCGATGGCGTGGAACCGAGCCAAGATGACGTGGCCCGTGGTGGGCCAGAATTCCAAGGAGTGTACTCGT
 CGGGGTGGCCGATCTGGCCAGGGCTGGCTAATTGGAAAGCTGGCAAGAACGGACCCGCAAAGGCCGGCGGGTGG
 GCTTCCCGCATTCAAAATCCGGCGCGTGTACCTGGCAGGGTGCCTGACCCACCGCACCAGCGCATAGAGGATG
 ACCGGCGCACGATCACGGTCCCGTGTACGGCCGCTGCCAGGAGAACACCCGCCGGTGCAACGCCACCTCG
 TGAGCGGGCGCGCAGATCCTGAACATGACCTTGTGCAAGCGGTGGGG (SEQ ID NO. 240)

Clone Rv230

:::::::::::Rv230SP6.seq::::::::::

TAACCTCAAGCTTCAAGTCGCNGTCCGACCCCTGTTGACGGCTACCTGAATCAACCCGATGCCCGCCGGCGTTCG
 ACCGCACAGCTGGTACCGCACCGGCCACGTCGCGGTGGTCGACGGCAGTGGGATGCAACCGCATCGTGGACCGAGTC
 GGTCGACTTGTACAGTGGGTGGATACCGGGTCCGGCGCCGGTGAAATTGAAACGGTGTGCTGCCATCCGGACGT
 GGCGGANGCGGCAGTCGTCGGGTGCTGACTATTATCTAGGCCAGCGGATCGTGGCTACGTTGCTACGTTAGTCGGCTCAGCGAA
 TGTCGATGCCGACGGCTATCAACTTGTGCCAACAACTTT (SEQ ID NO. 241)

:::::::::::Rv230T7.seq::::::::::

CCATGTCGCCAACATATCGCGATGTTGCGCTCGCCTCGCACGTGGCTGTCACCAAGTCACGTTAACGCC
 GCCGCACATGTCCTGCCGGGGAAAAACGTAAAAACGAGCGGGCAGTGAATGTCATGACACCGACGCCGCCGA
 TGGGCCAGGGTCTGGCAGATTGATCTGTGCGGCCAGTGCCAGCAGCGTCCGTCTGTCATACGGCCGGCGACGAGT
 TGAACCGACATGGGATGCCGTCGCCCTGAAGTCCCACGGCACCGGCCGGCTGGCCGGTCAAGATTCCANACT
 TGAAAGTACTGAAGCGCTGCACCCACAG (SEQ ID NO. 242)

Clone Rv231

:::::::::::Rv231SP6.seq::::::::::

CGAAAGCGTAAACAGCTCGCCGAGCCCCGACGTGCTGGATAGCCGGGGGAAGATCAATTCCAGGCAG
 CTCCCGGACAATGCGGCTCTGCTGGCCGCAACGAGGACTCGAGGTCAACCCGGTGGCGCAGCAACGCCGAGC
 CCGATCGCACAGGTTGGCCACAACCGGCCGCTGATGCCGGTCCGCAAGCCGGCAGTTGCCAAACCCAGCGTGT
 CNTGCTCNGCTCTNTACGGCGAAGAAGTGGCTGCCGTGATCACCTACCATGCCAGGATCTGCGTGTGTCATCACA
 ACGCTGCCAACAGGAGGTTGTG (SEQ ID NO. 243)

:::::::::::Rv231T7.seq::::::::::

TCCGCCACGCTCGGCCGCCGGCATACGGCGCTACCGATCTCCGCTCATACACCGGGTAATGCCGACGGTG
 CCGTTGCGAGCCGAAGGTGACGACGCTGATTGAATGAGTTCCAGGTCCAGCGGGTGGCGCAGCAACGCCGAGC
 TCAACGACGTCAATCACGGTGTGCTTCTACGGTACCGACCCGGTGACCGTAGTCGCCCCGGTGCCTCGGCGAGA
 AGCTGCACCGCCACCACCGCAGACCCGTCTTGCACGCCAGCCACCCGGATCGTTGGCCAAGGTAATTGGGT
 ATTCCATTGACGGGACGCCGACCC (SEQ ID NO. 244)

Clone Rv232

:::::::Rv232SP6.seq:::::::
 CATTCCTTAACAGTTGTTGGGCTGGCATGGTAGCCACGTTCTGCGGTCCACCATATCATCTTGGTCCGGTAGC
 GCTCGTCCGGGGTATGCTGCCGGGATTCTCGCTGCTATTACTCCCCCGAAGAACGCCACCGGTCCAGCGCGTG
 GGCGNCGCGTCCCATCACAAACTGAACCCCAACAGGGACATGCTTATGGTAGGGCGCGCCAAGGCGGAGCA
 ATCGCATCACTCGCTCTGCGTCACTATTAAACCCACCCGGACTTCACCTCCACCAACCCGAATGGCGCCCGTCAT
 TGATCATCTGGCGCACCGCGATAA (SEQ ID NO. 245)

:::::::Rv232T7.seq:::::::
 CGGTGCTCTGCAGTTGGTAGGCCTGCAGTTGTGCATCATGCCATGCCGCGGCCCTGTGGCACGCATGTACAGCAC
 CACGCCGCGCCCTCACGGCGAACATCGCCAGCGCGTCCAGCTGAAGCCCGCAATCGCAGCGCGTGACCAAAC
 ACATCGCGGTCAAGCACTCCGAATGCACCGGACCAGCACGTCGTACCGTCCGGCTGGGCCCCGCGATCTCGCCGC
 GGACCATGCGGACATGTTCCACGTCCCTCGTANATGCTGGTAGGCCGATGGCGCAAACCTCCATGACGAGTCGGA
 ATCCGCGCTCGCGACCCGCTCAATGTGCT (SEQ ID NO. 246)

Clone Rv233

:::::::Rv233SP6.seq:::::::
 CGGCATCTGGCGGCTGAACCTGTTCTGGCAACATGCCGAGGATGCCCTTCCACCGCGGTGGGGTGGCGTTG
 CATTACCTCACCGATGGTGCCTGTCAGGCCGGGATACCCGAGTGCCTGAAACATCTTGTGCTGAGTTC
 GTCGCCGCTGATGGCGACCTTGTCCGGTTGATCACGATNACNAATCACGCCANCACATTGGGGCGAACGTCGCGC
 TCGTGCCTGCCCGCAGCAGGCTGCCGCCGACGCAAGGGCCAACCAACAGTCCGTGGCGTGCATGACGTACCA
 CCATCGCGTGGTGTCAACCGCTTGGC (SEQ ID NO. 247)

:::::::Rv233T7.seq:::::::
 GCGGCAAAAATTGAAGCACTNTGGCACTNCCCGGGAGGGACAATCTGGCGGCTAGGGCTTCTCGCGGGAGG
 CCCGAACGTACTCGTTCAACACGTCGCGTCCGCCCTCGACCGCGAACATTCTGGATGGCAGCAACCTGTTAGCAC
 CCTGGCCGGGCGATGATCTGCAGCGTCCGGTAGTCGCCCCCGGGCTACAGTCTGAAACGCGATGACCATC
 GATGTGTGGACGCCGCATCGACNCAACGTTCTACACTGTGATATGTTGCCCTCGTGCACGGGTGGACGGTGGGT
 CTATCCCGGA (SEQ ID NO. 248)

Clone Rv234

:::::::Rv234SP6.seq:::::::
 CGCGTTGAACTGAAGGGGTGCCGCCGGCTCGAGCAGGCAAGCCATTGTTGATGCCGTTACCGAAGATCTTCGG
 TGACTGCCGCCGCCGGCAGCTCGGCTAGTGTCCGGCTGGTCGCCGCCGACAATCTGGCGTCCACGGTGGT
 CGGGGTCACTGCCCGCAGCAGGATTGGCAGCGGGNCGGTCAGCCGGGTGAACTCGTCAAGAGCTGACGCTGCGGTTG
 GGAGGCGAATCATGGTCGGTGCCTGACTAGGCCGGG (SEQ ID NO. 249)

:::::::Rv234T7.seq:::::::
 TGACAAACGCCGGCGATTACCCGCTACCGCAGCAGCATGACGCCGTAGCGAACACCGCCGGATGCAGCGCAGGTGC
 GTCGATGTGCTACGGAATCGCCCCGGCACCGCGATCTCGAGGATCACCAGTGCACCCCTGCAGCGCAGACCGAC
 GATTCCGTACACCGCCACGCCGATCAGGCCCTGGCCAGCTGATTGGAGCTGGCGTATATGGCGCGATGGTGACGAT
 GGTCATCGCCTTACATTGTGGCGGGCAGAACACCGCGTGGGGCGGGCGATGAAACACTAGGCACCANATCC
 CGGGGTCAACAGGTTGACCATCC (SEQ ID NO. 250)

Clone Rv235

:::::::Rv235SP6.seq:::::::
 CGCGGACATCCCGAACGAGGACACCGCAGCGCTTGGTGTGATCTATCAGGGCTCGCACCACGCCAACCGCTTCC
 GGCTACCTAGACGCCGT (SEQ ID NO. 251)

:::::::Rv235T7.seq:::::::
 GCATGCGGGTGATGCCGTTCTCAGTGCAGCGTACAGCGTGCACGCCGATACCCAGCCGACATGCCGTGCACGCCGGN
 GCCGGGGCGGGAAATCT (SEQ ID NO. 252)

Clone Rv237

:::::::Rv237SP6.seq:::::::
 CTCAAGCTTCAGNCCNTCTAACAGCGCTCGCGCGGATCGCAAAGATGCCCTTGCCGGCTGGGGCTTCTGCTC
 GGGGGTGTGACACCTCTCGAACACCTCGGCACCGACACCACCGCTGGCTGAACACCACGCCAACATCGGCAGC

ANATCTTGTATGTCTGGTGAATCCACGGTACTTGGAGTGGAAAGGCGGCCATACTGATCGCGCGGCCACCATGA
GCTAGCGCAGGAAAACCAGCAGCCGCTCACCCCTGCGCAGCAGCGTGGGTGATATGCCTGGCGCCC

(SEQ ID NO. 253)

:::::::::::Rv237T7.seq::::::::::

AGTCGAANGTCAGTCGGCTCCTCTCCGACTACGGCAAGAACTGGGGCAGCGTGTCACTGCAGAACAGCGGAAAC
TGGTGGCGCCCTAGGCAGCGAACGCTCACAAACGGCGGTGACCGCTCTGGTCGTGACCGATCGAGCCGTGCCAGC
CCGGCCCGCGTGCCTCAGCCGATCCACTGGATGCCCTCTCGGCGGTTCAATCANGTACAGGCAGCTCGCCACC
ATCGTGCCTGGGGCACGGTAGCGAGAACGCCACTTCACCGATTGCCTCGGTGATGxxxxx

(SEQ ID NO. 254)

Clone Rv23

:::::::::::Rv237T7.seq::::::::::

AGCTTCGGCGTGGCGATCGCGGTCAAGGCGCGCTTCGAGCACAACGAGCGAAGAACAGCTGGCGACGGAGCCT
TTATCGACATCCGTTCGGGCTGGCTGACCGCGCGAAGAACTGCTGGACCGTGTGAGTTTCACGACCTGACCATCGAAGATC
CCGAGCGCCGTCAGATGTCAGCCGCGGATGCGCCGGCGCTCAACGACATCTACGGCGCGAAGCTGGGTGAGCCCTTCACCA
CCGGCGGGCTGTGCTACTACCGCGACGGCTCTGACAGCGTGCCTGGCATGGCGACACCATTGGTCGCGGAGCACTG
AGGACACTATGGTGGCGATCGTCAGCCTCGGCGCCACCCGGCTTCCGCGTGCGGCGCGTGG

(SEQ ID NO. 255)

Clone Rv240

:::::::::::Rv240SP6.seq::::::::::

AGCTTCAGCTGATACTCGACCAGCCCCACTCGGGCAAAACGTGAATGTCAGCATCTTCACCCGTTACGGGCTANT
CGAGTAGAGACATTGATTAGCCTGAACGTAACCTCCGACGCCAGCTGACGAACGGGTATGACGGATGGATTCGTGGT
GTCGCGCCCGAGGTCAATTGTTACGGATGTTACGGGCTGATCTCGGGGCCGGATCGGGCGATGTTGGCGGCCGCGGGCTGG
GACGGACTATCCGACGAACCTGGCGTGGCGCGTGTGGTTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG
CGCGGCCCCGGCGGTTGGATGGCGCGGT (SEQ ID NO. 256)

:::::::::::Rv240T7.seq::::::::::

CTGGTATGGGACGTTGCTCCGGTAGGGCTACTGCGATCCTCCTCGTTGAGAGTGCCACCTCAGGGTTGGTAGGG
TTGGGTACTCGAAACCAAGTTACCCACCGTAACACCGTCAAAATATATCCGTTGATAGGTCAATGCAAGTTGATGT
GAGCTACATTGCAACAACTAACTAACCAACCGGTTGGGTTAGCGGTGATCCTGGCGTGTGGTCTCACCTGCGG
TGATAGCGATCAAATGAAGAATATGCGGAGTCTAGGGCGGCAGCGCCTGGCAGCTAGATCATGGCTACCGGGATG
CGGCCTCTGGTACGGACATGCGCGCG (SEQ ID NO. 257)

Clone Rv241

:::::::::::Rv241SP6.seq::::::::::

CTCGTGAGTAGCACCCCTGAAATTGGGATCGGCAAAAGGCGAATCACCGCGTGGCCACGACACGCCGGAGGGACM
ATCTCGGGCGCTAGGGCTCTCGCGGGAAAGGCCGAACGTACGGCGTTCAACACGTCGCGTCGCCCTCGACCGCG
AACATTGGGATGGCAGCAACCTGG (SEQ ID NO. 258)

:::::::::::Rv241T7.seq::::::::::

GGATCAACTACCGGCCAACGGTGATTCTGGGCGCGCTGACCGCGAACGACCCAGCGACACATTCAAGCAGATGGCC
AGCGCGTGGGGCCACGATGTTGGCTCGCGGCTACTCCCATGGTGGCGCGTGTGACATCGTACCGGCCG
ACCACTGCCGCCCTGGGTTACGCAGCGTGGCCCGAGCGGACGATCACATC (SEQ ID NO. 259)

Clone Rv243

:::::::::::Rv243SP6.seq::::::::::

AGGACCGTCAGCACGGCAGCTGACTCGCCGAGCAGTGGGAATCGCTCTGCAGCAAACCATTAACCTGCGCGACGT
TCGAGATGACCTTCTGAATGGACGGATCTACCTGCCGCGACGACCTGGACCGCGTATGCGTCCGCTCCGCTGG
CGACACCGGGCACTCTATGACCCGACGGACGGCTCGCGGTACTGCTGGGTTACCGCCGACGCCGACGGTACG
CGTCGGGACTGCGCTGAGTCCANCTCGACGCCGTAGCGCTGCTGTGCGGCCATGTCGATCTACCGCCGTC
CTCCCTTGA (SEQ ID NO. 260)

:::::::::::Rv243T7.seq::::::::::

CGACTCTGGGCCACTGCGGTCGATCTGGCGCCGCCCCGGTCGTGGAACGCCAGGTACCCGGCGCGACCGC
GGTCAGCGCGTGTGGCCAGCGTGTGACATGGAAGTGGTCGACGACGAGCTGGCGTTGGCAGCAGCCGGCG
GCGGATCGCCGAGGCGTATGCGAGCGGGCTGATGCCACCGTACTGGATGCTCTCCGGAACCTGCGGTGCGC
CTTGCAGCCATGCCAGCACCGCCGCCGCCGCGCTTCAATGCTGCCATAAACCTGATACCGGCCAGGTCACNA
ACCGTATCCACGGTCAACCC (SEQ ID NO. 261)

Clone Rv244

:::::::Rv244SP6.seq:::::::
 CACACGGACGGCGGTGCGGACGCAGCTGACGCGATGGTGGTCAGCATCGCGCCGGTCTGCTGTTATGCCACTT
 CGCGCCGCGAAATGCTGGTGGCGGGTGGTGGCGCTCGCATGGCTGGCTGGGTGCTGACCCAACCTCTCGAACCA
 CACCGGTGGTGGCTGGCTATGGCCTGCCATATCGGCCTGGTGTACN (SEQ ID NO. 262)

:::::::Rv244T7.seq:::::::
 CCGATATCGAGCCGATAGCTGGCGGGCTCGGGTGGTNGCCAGCGGCGTGCAGCAGAAAGTGTGACCGTCATGAAACA
 GACACCACCGCGGCCGTCGGCGCTCGTACCTGCTCGAGATCTCAGCATCCGAGCCGGTGTATCGCGCTTTCGGC
 GTGTAGTGGGTGCGCGCCGAGCCGGCAAACGCCGGCCGACACAACCCGGAACAGGAAGTCCGGTCACCGCGCC
 (SEQ ID NO. 263)

Clone Rv245

:::::::Rv245SP6.seq:::::::
 GCTTCAGGACAAATTGNATCCCTATGCACCCGTGTCACGCCGATGAGTGAAGACTGCACGCAATGCCGGAATCCGG
 CAAAACCCCTGACAAGCGAAATCAACCGGAGGCTGACAAGGCAACGTCGGTGATCCGTACCGCTGGTTGGACAAACG
 GCAGAAGGCGCCTCGTCCGGTCCATCTACGCCGAGCACACTGGTGATAGGCCATCGGCATCGGTGCGGCCACGGTGG
 AGACGAACGTCCCGNGGCGTCTGGGTGAGTAACCCGCCGACCAAGTCTCGGGCAAGCTGGTCAACATGGCGGCCACG
 TCTCCAAC (SEQ ID NO. 264)

:::::::Rv245T7.seq:::::::
 GTTTGGCGGCCTTATTGCACTGAGGTGTCATAATTGACCCACAGCGGAAATGCCGACTATTGCGAGGCCTCCTTCGCCT
 TGGCTGCCGGAGATGGGCTCCGCGGGAACCGCATGCAAGGTATATGACCTCGGTTTCGCGGTGCTACCGCGTGCCTTGC
 TCGAGGATGAACTCGGCGTTGAAATTGTCAGCCGGCCAATTCATCGAGCGCAGATTGTCACACATGGCCGGCGGCC
 ACATACCTTCACCGTGGATCTGCTCCACACGGACCGCCCTGCGGATCTGCTCACGGGTAAGGAATTA
 (SEQ ID NO. 265)

Clone Rv246

:::::::Rv246SP6.seq:::::::
 GCGCACTCCTCCTTATCGCTCCGCTCGCATCGCGCGCGGTCAAGGTGCAAACGCCCTCGGGGTGGGGTCCCTG
 CGGAGCACACCGGATACGGAGCGCAACCGCTCGCGTTGTGCGGGCAAACAAGTGTGCAAGNNCAATGCCATGTCCAG
 CAGCTTATCAGTGTGCAACGTGCGAACGTCGCCCTCGCCGGTGCCTGAATCTCTACAAG (SEQ ID NO. 266)

:::::::Rv246T7.seq:::::::
 CGCTGAAAGCACCATTGCGGGTGGCGCCGGCTCGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCG
 CGACACCACCCGGCTGCGTACGTGAGCCATACCGGGAGCTACATGGCTCGGCCCTAGTGTTCGGNCCTC
 TTGAGGTGAGGTGCA (SEQ ID NO. 267)

Clone Rv247

:::::::Rv247SP6.seq:::::::
 TGTAATTGGGATGGGAAAAAGCAAANCACCGCGTGGCCACAAACGCCGGGAGGGACAATCTCGGGCGGCTAGGGCT
 TCTCGGGGAAGCCGAAACGTACGGCGTTCAACACGTCGCGTGCCTCCGACGCGAAATTGGGG
 (SEQ ID NO. 268)

:::::::Rv247T7.seq:::::::
 CTTGGGCAACATGCTGAGGATCGCCTTTCAACACGCCGCGTGGGTGGCGTTGCATTAGCTCACCGATGGTGCCTTG
 TTGCAAGGCGCCGGGATACCGAGTGCCTGAAACCATCTTGTGCTGCAAGTTGTCCGCTGATGGCACCTTGTGCG
 GTTGATCACGATGACGAAGTCACCGCCATGACATTGGGGCAACTCGGCTTGTGCTTG (SEQ ID NO. 269)

Clone Rv249

:::::::Rv249SP6.seq:::::::
 GCATGCTCATATCTAATCTCCAGCCGTGGTTAATCAGACGATGAAAATTCATGCAGACGGTCCAAATAGAAAG
 ACATTCTCAGGCACCAGTGAAGAGGTTGATCAATGGTCTGTTCAAAAACAAGTCTCATCGGATTGAACTTTACC
 AACCTCATCCGTTCATGTACAACATTAGAACATGCTTC (SEQ ID NO. 270)

Clone Rv24

:::::::Rv24SP6.seq:::::::
 ATACTCAAGCTGATGCCGCCGAAACCGAGCGTGAAGCACGCCAGCACCACGCCGGTGGCGCCGGCGCCGG
 CGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCCGGCTGCCTACGTCTATCCATACCGGCC
 GAGCTACATCGGCTCGGCCGCCCCATTGTTGNGGCCCTTTGAGGTGAGGTCTATACCGATTGCGCATCCG
 (SEQ ID NO. 271)

:::::::Rv24T7.seq:::::::
 TCCGTACTGGTGGGTAACGCTTCGGTGCAGTGTGCGAGTGATAGATGACGACGGGACCTCGTCGGCATCTTCCATA
 GCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGTAGAAGGTGGCAGCGCTCGGCATTGGTCATCGGGATA
 TGCCGCTCGGGACGGTCAGAACCTCGGGTCCG (SEQ ID NO. 272)

Clone Rv251

:::::::Rv251SP6.seq:::::::
 GTTCTCGCAGATTTCGGATTAGCAGGGATGGTCTCAATTGGGTATGCGGGGAAGGGCCTGACATTGCCCGATTAGC
 TGTGATGGACCGGGGTGATTTGATCACGGAAATGGGTGTTATNCAGGTGCGACGCTTCATCCGGGCGAA
 CG (SEQ ID NO. 273)

:::::::Rv251T7.seq:::::::
 GGGTGTGCCTGCTGTGATGCACGGCATACGGACATCCTTCCCTGAAGACCCGCGGTCGAACAGCCACGTGTCCATC
 ATCANGGGTCAACCCGGCAAGGGCAGCGCACGCCAAGTTCGCCACCGTTAACCTAGTGTGTTAGCTTCAATT
 GCTGCCAGAAAACAGCTGGTGGNCGTTAGGAATGAATTGAAAATCAACCGATTGGTGCCCGTAGGTGTCCCTGG
 CTG (SEQ ID NO. 274)

Clone Rv252

:::::::Rv252T7.seq:::::::
 ACTACCCGGCCAACGGTATNTCTGGCCGCCCTGACNGCGGAACGACGCCAGCGACCACATTCAAGCAGATGGCA
 GCGCGTGCCTGGGCCACGANGTTGGTCTCGGCCGCTACTCCCANGGTGCNNCGTATCGACATCNTCACCGCCGCAC
 CACTGCCCGGCTCGGTTACCCAGCGTTGCCGCCGAGCGGACGATCACATCGTTTATTTNNNTTNCNGGAAT
 CCCTCGGGCCGCTGGCGGCTGATGA (SEQ ID NO. 275)

Clone Rv253

:::::::Rv253SP6.seq:::::::
 ACGTCGGGANACTGTTCGCGTTCATCCTCGTCTGGCGGATTGGTCTGCTGCGCCGGACCGACCGATCTTCAGCGGGG
 GGTACGCTCCGTGGGTGCCGTTACTCCGATCGCCAGTGTGCGCGTGTGTTGCTGATGCTGAACCTCACCGCGT
 TGANTTGGATCGGTTCGGGATCTGGCTGGTGGCCGGAACGCNATTATGTCGCTACGGGCGCCGGC (SEQ ID NO. 276)

:::::::Rv253T7.seq:::::::
 GCTCAAAGGCACTACTGGCACCAAGGCCACACGTACCTGTGACTCCTGCGCCGACCCGCCAGGGTCTGGCGTTA
 CACCGAACGGCGAGCCGGAGTTGGTACCATCGAACAGACAAGGTGCATGGCGGAGTTGTTCCGCCACTCGTCC
 ATGACGGGTC (SEQ ID NO. 277)

Clone Rv254

:::::::Rv254SP6.seq:::::::
 CGATACCGGCTGTTACCGAGACATCCACCATGCCACCGAACATACCGCACGCCGAAATCGCACAAACAGCTTGACG
 CCTTGCAGGTTCGCATGGATTGGCGACGGCTCTGACGGCGTGCACCTTGGCAGCCTCTACGAGCTCTCGGAAT
 CACTTGCCAGCAGGGGTTCGATGAGTGTACACCGAACCTCGATATGGCGCAATCCTGGCCGACACATCCAAC
 CGGGTGGTTGTGCTGCCGCCGGTGGGTCNGCAANACACTACCGCGGCCGCTGGCGTTGCGCGCCGGCGAAT
 ATGGCCGCACTGTGGTCG (SEQ ID NO. 278)

:::::::Rv254T7.seq:::::::
 CGTCGTCGTGGTATGCGATAGCCATCCCGTGGGCTACTCGCCATCACCAGTCACTGGCTGCCGAAAGCCGCC
 GGCATTTCCGCTGCACCAACTGACCGGGGCCAACCGGTATTGCTTACCGCGACAACCGGGCCACCGCGATCG
 GCTCGGTGTACANGTTGGCATCGACGACGTACGGGCCGGCTACTGCGACGACAANGTCGAGCGTGCNGCTG
 CAAGCTGGAGGTGCCAGATTGACCGTGGTCGGTACGGTATCAACGACCTCCGGCTTAGCGGCCGCGATGTCGAT
 CGCCATGGGCAGCGCCGAC (SEQ ID NO. 279)

Clone Rv255

:::::::Rv255SP6.seq:::::::
 GCACGCAATCGAAGTCACCCAAACCGGGCGGGCCAGCGTCTNACGCCACGTCNACAGCCGAAACCTCAACCCGGCC
 ACGGCGAGCTCTGATCAAGGCCAGGGCATCGGTGTCTACTTCATCGACACCTACTCCGCTCCGGCAATATCCGC
 CGCAACTCCGTTCGTCATCTGCTCCGAAGTATGCGGCACGGTGGANGGCCGAGGGGTAC
 (SEQ ID NO. 280)

:::::::Rv255T7.seq:::::::
TCGACTGTGTGCCACAGATCACGCCCGCATGCCGAGCAGGAAATGCGTCGAATTGCCGCCGGCCGGCAT
GCTCGGGTTGCAGACGGCATTGTCGGTGGTGCATAATGGTGGCCGGCTTGTGANTNGCGCAGATATCGC
GCGGGTGTAGTGANACCAGCGTGC^(SEQ ID NO. 281)

Clone Rv257

:::::::Rv257SP6.seq:::::::
GAACCTGACACCCCTGGTCACGGGTGAGCAGGACTTGATTCTCNCTATTGGTGGCGCTGTTGAGCACACCACGCC
GCTGACGGCCGTCGCGTCCCGTGTGCTCGGCTGGTGGAGCGCGCTGCCGCCNAACATCNTAAATCAAGCGT
ATTGTCACACAGATATCATCAATGTCGGCGCTGGACTATTCAAATCATCGATATACTGGTGACTCTGGCCTTCGCCAT
CGATCAATGGCGATAGTCACGCAAATCGTCACGGACATCGTCGGCGTCCAGCTGGCCCGTGCACACAGATGCTGCAA
CCCATCGGGGTTGATCACCGCGGTGCTCGCGATGGTCCACAATTGCGGTCCAAGCCCNAACATCCCGGGCAT
GAATTACCGGCATGCGC^(SEQ ID NO. 282)

:::::::Rv257T7.seq:::::::
CTATCGTACCCGCGCCGGTCACCTCTGGATATCGCGGCCCTGGCAAGGGGGCGTCCGAGGGAGCCGGCTGGTNA
CAAGTCTCGGCTCATATCCGCGAATGCGACGCCATTGTCAGGTGGTGCGGGTGTTGTCGACGACGACTGACTCA
TGTACCCGGACGGGTCGATCCCCAGTCGACATTGAGGTGCTCGAGACCGAGCTGATCCTGGCAGATCTGCAAACCCCT
GGAGCGGGGCCACGGGCCGGCTGGAGAATGAAGCGCGACCAACAAGCGCGAAGCCGGTCTACGAAGCGGCACTGCG
TGCCCAGCANGTGCCTGACGCCGGCAAGACGCTGTTGCGCCGGGGTGGATGCCGCCGTTGCGCAGTGAACACT
GCTGACCACCAAGCCCTTCTGT^(SEQ ID NO. 283)

Clone Rv258

:::::::Rv258SP6.seq:::::::
TACTCAAGCTTCAGGCCACGTCCGCCGTGGCAGCTGACCTCGAGCGCCGAGTTGACTCGACATCGCCG
CCGGCGCATGCCACATGAAACCGGCACTCACCACAGCCGTCGGACGTCAGGTCGATGACTCCGCTTCAGCACC
GGATCGTCCGGCAACTCGCGGCCCTGGCCTGCGAACGGCACACCCGCTGTCGGGCNCCCGCGCGGAACGGGC
TCATCACGGTGTGCGAGCCGGTGCACCGCTACCGACGCCGTC^(SEQ ID NO. 284)

:::::::Rv258T7.seq:::::::
CCGACATCGAGTGGGCTCGCAGTGACTTGGCAGCTCCAAGCCACCGGTACCCGCCGCGGGCAAGCCAAGGACGACG
ACGGCCTGCCGGATAGCTGCGCCAGCGCTTGCGCCAAGTGGCGTCCAGCGTCGCCACGATCGTCAAAGAGCTTCATC
TGCCGAGTGTGTCGCCATCTCATGGCTCCAATATGAAATTAGGTCCCTGGGCCACTGACGACAGTCCCTCAGCGAC
CGGATTGCGCATCCGCCCTGTACGTAACCGCAAATCCGGGTTGCGTCCGCCGAAGCGAACCTGGCGCTAC
GTGGTGGTTCACTCGGCCGTGCGCACTCGGATCGACGGGCCATGGTGGCCGGGCCGCGCTTGGTCATCCG
ATTGAGT^(SEQ ID NO. 285)

Clone Rv259

:::::::Rv259SP6.seq:::::::
ATACTCAAGCTTGTGCGGGTAAACCGCACGCAGGGCGGTGGTGCGGTGTCAAAGACACCCACACTTCTTGCGGTT
GGTGTCTCGACACCAGCGAGCCGACCCATGCGCGCTAGATCGCGATCAGCGCTCGGCTATGCCCTGGT
GCCGCCACCGGAATCGGCCAGCCGAATGGGCCAGCGTGTGCCAGCATCAGTCCGGCGCCGGCACACCAGTGA
CGGCAACGGTAAATCGCGTGGCGAACGCCGGTGAACAAACGCGCGGGCATCTCGCCGCCAACGACCGCCAGGC
AGGGTGCCTGGCCATCATCCGACGCCGA^(SEQ ID NO. 286)

:::::::Rv259T7.seq:::::::
TGGACTCATAACGATCGGGTCAGCGACGCCAACACGAACGGCCGGACGAGTGGGCCAGGGTCGCGCTCCCTACA
AACAGGATCGCTGCCGAGCGACAGGCTCCGGTGCAGCGTCCGGCTGCTCCTCCAGCGTCCGGTCCCGGG
TCGCCGGCAGCGCTTGTCTCCATACTCGCCCCCTAATCTGAGGCCAGCCGTAACCGCAGGCAACCTCCAAAAAA
TGCAATCCCCAAAATGCAATGCGTCGAGCTATTCTCACACCGACCGCTAGTTGCGGATCAGAAATCCGTTGGCGC
GGAAGTCCAGCGAATTGTTCTCCGCTCCGATCATGCTTGTAAATCGTTGGAAATCATCCTCATATGCCCTGATC
GCTCATAGGTCAAGCCAAACCGCAGGATGGGTGGC^(SEQ ID NO. 287)

Clone Rv25

:::::::Rv25SP6.seq:::::::
CTTACACTTATGCTTCCGGCTCGTATGTTGTTGGAATTGAGCGGATAACAATTACACAGGAAACAGCTATG
ACCATGATTACGCCAACGCTATTAGGTGACACTATAGAATACTCAAGCTTAGTGGTGCACGTAAATTGTCAGGT
GACCGATCCCTGCTGTCACTCGCCTCACAGCGACCAACCGCTGGCGTCAAGCGGGCACGTGCGGAGCAGAT

GAGGAATGTGCGACGTCTGATGCAGCCTGTCAGAACACCGAGACCCCTCGACGAACCTACGATCGAAACCGCTTAGGC
 CAACCGGTGACGGGGTGTCTTCCGGCTAGGGCGCTATCGTCCGAAGGCCGTGGTGGTATCGCCTCTGGG
 TCGCCTGGGGTCTGCTTGCACGGTCCCTGGACCGATCTCCAGCGGATCCAGTGGCGATTCTGCC
 ATCGG (SEQ ID NO. 288)

:::::::Rv25T7.seq:::::::
 CAGGCATGCAAGCTTGCATGTATCAACACGCCGTTGCGCAGCGTGAGCCGATAGTTGACATCCGGCTCGGTGAAGGT
 GAAATCGATGCCAGGTGAGGTCCATGCGCTGGGCCATTGATGCTGATGCCAGGACGTCAAAGATTGGTCCGG
 CGTCAGCTGGCGAAAAACGTGGGCGCCGGACTTGCACGGTGCCAGCTGCCGGGTTCCCGTGCAGCTCGCGGGCCCC
 GGTCAAGAAAGAAATTGCGCCAGGTCCGACACTCCGCGCCGTAGGCCAGCTGCTCACGGTGTGGCATATAGCCCGG
 GGCCGAGCGTGTGCTGCTGGCGAACACCGCATGGTCAGAAGCGTGGCCAAACGGAAATCACTGCGTCAAAG
 CTTGCCGGGCACTCCAGCACTCCGTC (SEQ ID NO. 289)

Clone Rv260

:::::::Rv260SP6.seq:::::::
 ATACTCAAGCTGACCGACGCTGATCGCACCGCACGCCGGAACCTCAAGGGCACTACTGGCACAGGGCCACACGTC
 AACCTGTTAACCTCTGCCGACCCCGCGAACGCTGGCTTAACACCGAACGGGCAACCCGGGAATTGGGTT
 CCATCAAAACAAATAGCAGGTGCTGGCGAGTGTTC (SEQ ID NO. 290)

:::::::Rv260T7.seq:::::::
 GTCGTCGTGTGCTGGGCGTCCGTATCAGCACGCCACGAAATGGGCACAAGAAGGATTCCCTGGAACGGTGGCTGTC
 CAAGATCACCCCTGCCAAAATGCTACGGGACTTCTACATCGAGCACACCGTGGCCATCACGTCCGGTGTCCA
 CACCGGAGG (SEQ ID NO. 291)

Clone Rv261

:::::::Rv261SP6w.seq:::::::
 ATATGCCTTGCTGAGCTTTCCGATCGCAGCGAGTCGTACCCGCCGGTACCTCGTGGATATGCCGCCCTGGTC
 AAGGGGCGTCCGAGGGAGCCGGCTGGTAACAAGTTCCGTATATCCGCAATGCGACGCCATTGTCAGGTG
 GTGGGGTGTTCGTCGACAACGACGTGACTCATGTCACCGGACGGGTGATCCCCAGTCCGACATTGAGGTGTCGAG
 ACCGAGCTGATCCTGGCAGATCTGCAAGCCCTGGAGCGGGCACGGGGCGCTNGAA (SEQ ID NO. 292)

:::::::Rv261T7.seq:::::::
 GACACCCCTGGTCACGGTGAGCAGGACTCGATTCTCGTATTGGTCGGCGCTGTTGAGGCACAGCACGCCGCTGAG
 GCCGTCGCGTCTCGCTGCTCGTGGTGGAGCGCGCTGCCGCCGAAACATCGTAAATCAAGCGTATTGTC
 AACAGATATCATCAATGTCGGCGCTGGACTATTCAAATCATCGATATACTGGTGACCTGGTCTTCGCCATCGATCAA
 TGGCGATAGTCACGACGATCGTACCGACATCGTCTGCGTCCCAGCTGCCGTGCCAACAGATGCTGCAACCCATCG
 GGGTGGTATCNCGCCGGTGTGGTCAACAAATTCTGCGGCTCAAGCCCAGAACATCCGGCATGAGTT
 ACCGGCATGGCGAACGGCTGGTGCCTGGCAAACCGCGGCGATCGAATT (SEQ ID NO. 293)

Clone Rv262

:::::::Rv262SP6.seq:::::::
 TGTAGAAGGTGGGTCCGTCACCTCGCGGCCGGCGATATGCCCTGCTGGCTTGCTCATTTGATATCCAATC
 TATGGGTCGTGGTTACTCAACGGGCCAGCTGGCCCTCCCACGGTAGGGCCTATTGACGGTGTGTC
 (SEQ ID NO. 294)

:::::::Rv262T7.seq:::::::

CCCGAATCCGGTGGCGCGAGGGGGCCTGGCAGCTGGACACCTTCTAACCTGTTACCGGTCACTGTTGACCCCC
 AACACCTTAAACGACGTGGACGGACGTTACATCGGATTGACGGTGTCACTCCACAGCGTTGCCATTGGCACACCCAC
 TACGCCAATTCTCCGACTGGGACACCTACCGCAGCCTGGGGACTGCAGGGACTGTTGTTCCCGAACGGGCCATC
 GACATGATCCAGTCGTTGGTACCGACGGAGCAGACTGGTGCATCCGCTGGCGCTGGCGAACATCCGGCAC
 CGGCATGAT (SEQ ID NO. 295)

Clone Rv263

:::::::Rv263SP6.seq:::::::
 TTGAGATGCTGGTCGGGATGCCGATGGTTGGAACATGGTCCCTGGCGTCAATACGCGGAGCGCATGAGCTCACCG
 GTTCGGAACACGATCGCAAGAACCTCGCACTGCTGGCAGATGGTATCTCGATGGTTGAAATTGTATCCAACTC
 TAACTGTGCTATCGGATCTGCGTGAATA (SEQ ID NO. 296)

:::::::Rv263T7.seq:::::::
 CGTAATCACGATCCCCTGAGACACTGACCTACGGCGAAGTGACTCGCTGCTGCTATGCCGACACCCGATTCC
 ATACGCTGCTGTACACGACGGCGGGCGTGGCCTCCATCACGCTAACCGCCGAAACAGCTAACACCATCGCC
 CGCCCATGCCGACGAGATCGAGGCCCTATCGGGTGGTGAACGCGACCAGGACATCAAGGTATCCTNCTGCGCG
 GTGGCGGGCGCCCTCTCCGGCG (SEQ ID NO. 297)

Clone Rv264

:::::::Rv264SP6.seq:::::::
 CAAGCTTAAGCTGGTCTCGGCCACTCCATGAGCGTAGTCAATGGTCTGCACGGCGAGGCCGAACTGCCATAAA
 CATCCCTGACGAAAGTCTCCGGCAAGCGATTGCTTCTTCGGCCGTTCTGTGGATTGTCGATAACCCGGTCCCT
 CATGCTGGAAGTTGTGCGCACTTTTCTTCGGATGTGGCTAACGACTCGTCATTGAGCAAGAAGTACGTGACA
 GGCATCGTCCGCCGGCTTCAGCACGCCGGAGATCTCGTCCAGATAGTGTCCACGCCGGNGGAAACATGTGGTGA
 AACACCGAGGTNAGAAACACCNATCCAACGACGCATCCGGATATGGAAAGCGAA (SEQ ID NO. 298)

:::::::Rv264T7.seq:::::::

TATGGTCTTCGTCGACCAGTACGCTGAGGCGCCATGAGCCAGCGACTGAAGCCGCGCCATGCCCTGCACGGCCCGCTC
 ATCCAGCGAGGCCGACATCTCCGCAAGATAGCCTGCCCTCGCGCGCACGCTGTCGGATCGCGTCCGAGGCTCGTC
 GGCAGCGCACCGCAGCCGCTCGTCATACCATCGGCATCCAGCAGTTGGTAACCTAACCGGGTCCGCTAGCGG
 CGTATTGATTGAGCAACAAATACCGATGCGCTGCAACTTCCAGTCCGATGCCGCCACCTCCGTGCAAGTCAC
 TGGCTAGCCCCCGTCATGCCGGTTGTGTCGATGCCAGCGCAGCGGCTCGTAAACCTGCCGCTCAGCTCGTGG
 (SEQ ID NO. 299)

Clone Rv265

:::::::Rv265SP6.seq:::::::
 GCTTAGCGGTCTGCTCGAACCGACATTGCGTGCACACTCATGAGCGGGTGGCGGTGCGCTTACACATCT
 (SEQ ID NO. 300)
 :::::::Rv265T7.seq:::::::
 GTATCTGGCGCCCTCTGAATATCCTTGAACGTCGCCGGTGCACCCAGATAGATCGCAGCGCCCTGCAATGGAGTTC
 CCTTTATGCCCTCTAGCCTCCGCTTGATCGCTCGACCCGAGAGATGCCCTCGGGATCTCCCTCCA
 (SEQ ID NO. 301)

Clone Rv266

:::::::Rv266SP6.seq:::::::
 CTTCACGCCATCCCGCACCGCGAACCGCAGCGTGGCGACAAGGTTCGGTTGGTCGCCGCGCTGGCG
 ATATCAGCTACCCGGTTTCGAGGTGTTCGCGCACGGACGGTGCAGACATTCTGAGCGTCCCTGACCGGCGCG
 ATTCCGCTTCACACATCGTACGCCGTATTCGGCGTACCGCTCGGCCGAGTCGAAGGCGCCTGAGCTAAAGCC
 GGGCATTGCGCAGTGGTAAACAAGTTCGGTGACTCGGTTGACCGACTCGACGGGCTCGATCTGGCGCGCTGGACC
 GGTATCTGCGTCGCTGGGATCGGGCNACCGCNANTTGCCTGCGANCTGATTCCGGTGGAGCTCCAATCTGACTT
 CCGG (SEQ ID NO. 302)

:::::::Rv266T7.seq:::::::

GCAGCTACCGACCCCTAGCGACGAGTGTGTTCGCAGCGTCGAATGTGAACGTTGGCGTGATTGGCGCGGGTTCCC
 GCTCTAGCGCACGTTGGCGCCGAGGGGGTAGTCCCTGGTTAAGCAATGTCTGGTGCCTGCCAGCAGCGCGCATG
 TCGCCAACCCGTCACCGCGTTGCGCATGTCGGTACCGACGGAAACGACGGCGCATCCGGATGTTCTGCGTCCG
 GATCCTTCGATACGGGAACGACCCCCCGCTCGGTACCGCGATACCAACGTCCTAGCCAANGCTACNGTCCGGCG
 CGCGTCCCGGGCAACACGTCGAAGCTGATGAANTAACCAACCTTGGGCTGGTCCAAGANGCGATCTGGACTCTT
 AACCGCTGATNCAA (SEQ ID NO. 303)

Clone Rv267

:::::::Rv267IS1081N60.seq:::::::
 TCCCCATGGCGCCGGACCGTTGAAAGTCCAAGCAGGGTGGGATGGAATCGACGGACAGTTGAGCGCCGTCGGTGGC
 CGTGGTCAGCAGCTGTTCGCGAACGACCGAGGTACATCCCTCGACATCTCACCGACGTGGCACGGCGACATCAAC
 AGGAAGATTGACGAATCCCTCGCAGGCCGGCACGTCCGCAGGCCAACGACGGGCAACTACGGGCCACCGCGATCCTCCG
 CTCACGCACCAGCCAAGCCAGGCTACGCCACCAAGTCGGCCGCGCTCCCTCGCCCCCTGGTCTCCGGGGCCTT
 GTTAAACAACCTACCGGAAGTCCACCAATCTCGCTGCATCTGACACCGTCCGCCACTCCCTCCTCCGCCCTC
 TCCACACACACACCTCTGCATTAAGGTACCGAGCGGTCACTTTCGTCGGACGAAATTGCAATCCGGCCGCTCG
 CGGCCAGAGAT (SEQ ID NO. 304)

:::::::Rv267SP6.seq:::::::

CGGAAAGTGGATACTCCCAGCAGGTAGCAGGTGCCACCACGCTGGTCAGTGCCTGAGCTCGCTTGCCTGCGCTGC
AGCAGCCAGTCCGGAAATAGCTGCCCTGGCGCAGCTTGGGGATCGCAGCTGATGGTGCCTGACGGGTGCGCAA
ATCACGGTGGCGTAGCCGTTGCGCTGATTGGACCGCTACGCTGCCTGCCTAGCCGCCCGCACAGGGCGTC
GGCTTCAGCCCCATCAAGGCGCGA (SEQ ID NO. 305)

:::::::::::::Rv267T7.seq:::::::::::
GGCCGAGTCCAGCACTTCGCACTATGTGCAGACAAAANACCCGGTGGTCGCCCGCTGCCAGCGGGCTGGCAACGGC
GCCGGTGTACCGAGTGGTGCAGTGGCGNAGTTGCCGACCGCAGTTGCCGCGGGCTACTACGAGAAGGGCTGCCGACG
TCATCAGGTATCACGTGTCGATGACGCTGAGCGTTAACCTCCCGACCAAGACGGCAGCTGCCGATGGACCCCGCT
TGTACCTGGTGGCGCAAGCTAACGCCGCCGACNGCTATCGGTACTCGGTCGAAGCGCAGCCGGGTCGCAAGCGC
TAGCGGGCAAGGTCGCGACGATCTCGGTACCGTACCGCCTGACCAACTACGGCCTGCTGCCGCCACCGAATAGTGN
GCTACCCGGTGGATTCCACGGGACATGTGGTGGACCTGCCGCCAGCGGTGGAACGAAAGANGCTGGCT
(SEQ ID NO. 306)

Clone Rv268

::::::::::::Rv268SP6.seq:::::::::::
AGCTTCAAGGACATCGTCATCGCAGCAGGAAACCGCGAGCTAGGTGGCATCCGGGAAGCAGTCGACACCGTGGCGCC
GAGCGCCGCTGCCGGCAGGGCAGATTAGCGGGCAGATTAGCCGCGCCGCTCCGGCTCCGATTACGGCGCCCGAA
TGGCGTCACCGCTGGTAACCACGCTTGCCTGGCGCCCTGGCGGGCTGCCGATCAGGTGGTATATGCCGACAAAGCC
TGCCTGATCGGTATCACCAACGGTACAGCAGCCGGTTGTGCACCATCGCNAACGCCACCCGGTCTCCGGGCTGT
CAN (SEQ ID NO. 307)

::::::::::::Rv268T7.seq:::::::::::
GCTCGCGGTCCAGCAGCAGACGTGTCGACCCGACGCCGGCCGGTACCGAAACGGATGGCCCGCCGATGGC
CGCGCCACGGCGTCTGCCCTACCGGCCGGATACCGAGCCACACCTCGCGGAAACGCTGAATGCCGCGCAGGGT
CAAGGTGATTCCGGCGTGGCGCGGTTTCGCGAATCGTCCACCGCCACCACATCGGGGTGCTCTCGAAGACGCCGGG
TGTGCGGGAACAGCGAGTTAATGTGGCCCTGGGCCCATGCCAGCAGGTGGACGTCGAAATTGGCCGGGTCACC
TGGTGCAGGCACTGGCGGCC (SEQ ID NO. 308)

Clone Rv269

::::::::::::Rv269SP6.seq:::::::::::
AGCTTGTGATCGTCGGCAGCGTCCGGCGAGTCAGTCGAAAGCCAGTCGGCTCTCCCTCCGACTACGGCAAGAAC
TGGGCGACGGTGTCACTGCATACCAGCGGANACTGGTGGCCCTAGGCAGCGACCGCCTCACAAACGGCGGTGACC
GCGTTCTGGTGTGCACCATCGAGCGTGGCCATCCGGCCGTGCCGTCAGCCGATCCACTGGATGCCCTCTCG
GCGGTTCAATCAGGTACAGGCGACGTTGCCACATCGTGCCTGGGCA (SEQ ID NO. 309)

::::::::::::Rv269T7.seq:::::::::::
TTGGTGTATCGNCACGACCCCGAGGCAGTTCTTCACACCGAGGTGTCGCAAGCTGGGCTGGCCTTCG
CCGCCGATCCGTCTCAGCAGCTGGCGAAGCTGTCGGGAGGGAAATTGCAAGGCTGTCACGGTGCTGCTTACTTG
TTCACCAACGACTACTAATGGGATCTGCTGCTGTCACAGCGCTGGTCAAGANGCCGATGTGATGGCGCAGATCGAC
CTGCGGGTGACCACATTGGGCTTAAGGGTGTGATTTGGTAGAACCTGACGCACCCATCCACGTCGGGTTGGTC
CCCGAAACAGCCAGACCGA (SEQ ID NO. 310)

Clone Rv26

::::::::::::Rv26SP6.seq:::::::::::
GGCTCGTATGGTGTGGAAATTGTGAGCGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCT
ATTAGGTGACACTATAGAATACTCAAGCTTGTATTGATCATGATGATCATACCCGAAGTGTGGTAGCCGCG
TGGTTATCGTGGTACCGTGTGCTTCCATGGCGCCCTTCCGTTGGCTATTGGTCTGGCAGGACATTCTGG
GTATCGAGTTGACTGGATGGTGTGGCGATGTCGGTGTGCTCTGGCGGGATCCGACTACAATCTGCTG
TGATTTCGGTGAAGAGGAAATTGGGCCGATTGAAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAG
TGGTGCAGGGCTGCCGCATGGTGTGCTTACCATGTCGTTGTTGTCAGCGATTGCGAATT
(SEQ ID NO. 311)

::::::::::::Rv26T7.seq:::::::::::
CAGGCATGCAAGCTGGCGTGCCTCCAACCCGAATTGGCTTCCGGCCATCGTGGAGGACGGCGTGGGGTGC
AACGACGACGTCGTCCGGGACACACCTCGATGCTGCCGATGGACGCGGTGAAACGCAAGCAGCTGAGCTA
CAACGCCGCGGGAACGCTTCCGCCGGCGTGGACCGCATCCGTTGACCGGGGGATCGCGGTGATGTCGATGAC
GGCATGCCACCGGAGCGACGGCCAAGCGGGCGTGCAGGTGCNCGGCGCACG (SEQ ID NO. 312)

Clone Rv270

:::::::Rv270SP6.seq:::::::

GGCATCTTGGCCGCCATGTTAGCCACACTGCCACCGCTATAAGCGATGCGCACCGTCCCTGCCAGCACATTGCCGC
GCTCCTCCCTGGAAAGCAAGATAACCAAGCTATGCCGTGGTTGTGGTGGCTGGTTGGTTGGTAACTTGG

(SEQ ID NO. 313)

:::::::Rv270T7.seq:::::::

TCGGCTAATAATCGTCGACGCCGCCCTCCCTCGAATCGCCTTGGCGTCGCCGGGTTGTCACCGGTGATCATCACGG
TGCGGATGCTCATTCGGCGCATTCGTCGAATCGTCCCGTATGCCACCTTGACGATGTCCTTCAGATGGACGACGC
CGATGGCCCGCGCCTGCTGTTATCGGTCATTCCGCAACGACTAGGGGTGTCCCCCCGCCGAGCTGATGCCGTGAC
AATGGCACCCACCTCCTCGGTGGGTGGCACCCTGATGCCAACCCACTTCATCACCGCAGCCGGCACCTTGC
ATTGCACGGATG (SEQ ID NO. 314)

Clone Rv271

:::::::Rv271SP6.seq:::::::

CTCAAGCTTGGAGGCCTGGCGATCGGGTCCAAGCGCGCTCTCGAGCACACGAGCGAAGACNGCTCGGCGACGGA
GCCTTATGACNTCCGTTGGGCTGGCTGACGGCGCNAATAATGCTGGACTCGTTGTCACGGTGGCTGG
GAGCCGAGCGCCGTCAAGATGTACGACCGGGTGGCTATGTGCCGCGGTTGGTGAGTTCCACGACCTGACCATCGAAG
ATCCGCCGATCCGCTGCTGGCGGGATGCCCGGTGGCTCAACTAATTCTACGGCGGCGAACTGGTNATCCCTCN
CCACCGTCGG (SEQ ID NO. 315)

:::::::Rv271T7.seq:::::::

CCTAGGTCAACCGTACCGTCATCGGATCGGGTGCACCGCACAGATGGACTGGAGCTCGCGAGGTGATCGCCTATG
CCTCGGGGGGGTGACGCTGACCCCGGGTGACGTGTTGGCTCGGGCACGGTGCACGCTCGTCGAAGCAC
CTCAGGCCACCGGAAATCATCCCGGCTGGCTGACGACTGCGACGTGTCACCCCTCCAGGTGAAAGGGCTGGCGA
GACGATGCAAGACCGTCCGACGAGCGCACTCCTTCCGTTGGCTCTCGGCCGAATCCGACGCCAACCCGACCG
GCGGGGTCAACCGGACCGACGCGGGTGCCTTACCCGGGCTGCACAAATCCGACGGTATGGCTTGGAC
CTGCGACGGGGA (SEQ ID NO. 316)

Clone Rv272

:::::::Rv272SP6.seq:::::::

AGCTTGGCGTGACACCAACACAGGGCACTTAAGATGGCAATGCCGCCCTACCTGACGTTTTCGCGATGTCAGAGGA
TGCCGAGGGGAGAACATGCGAGCACGCCGCTGACGTTGCTCACCGCTTGGCGGGGTGACATTGGTGGTTG
GGGCTGCGAGGGCCGAGCTAGGCGAACGATATAGCGCGGCCGACCGCATTCTGCTCGACCGCAAGCGGACCTCA
GCCGAGCCGGTGGAGCTACTGCTGCCGCCATCACGCCCTAGGGCTCCGGCGGGCTGCCGAACGTCGGTTGG
CGAACACTGCCAACCGGGTCCGGCAGGCAACCGAT (SEQ ID NO. 317)

:::::::Rv272T7.seq:::::::

TCATGCCGTTGGACCGACCATCGGAGTTAGTTGCCGAACCGCGGGACCAACGCAAGCACCCGGTCCCTGGTCGCGCACC
GCGTGGCCAACCGCTTGAGCACCAACGCCGAGCCCTGCCGCGACGAATCCATCCGTTGGCTGCAAGCTG
TTGCATCGGCCGGTGGTGCAGCGCCGACCAACTTGGACAGCGCGATGGCGTGAACGGTGACAAGGTGAGCTGCACC
CCGCCGCAATGCCACGCGTTTACCGCAGGCAAGCTGACACGCCAAGTGAATTGCCACCAGCGACGACGAAC
AAGCGGTATCTACGGCGATGG (SEQ ID NO. 318)

Clone Rv273

:::::::Rv273SP6.seq:::::::

GGTCGACTTCTGCAAGCGAGGCTACACCGTCGTCGTTGGTATGCCATCCGTCGGCTACTGCCAT
CACCGATCAGCTCGCCCCGAAGCCGCCGTTGGTATGCCCTGCGACCAAAACTGACGGGCCAAACGGTATTGCT
TACCGCGACAACCGGGCACCGCCGATGCCGTTGGTATGCCCTGCGACCCATGATGCAAAACCTTC
(SEQ ID NO. 319)

:::::::Rv273T7.seq:::::::

AATCCGAAATCTGACCGATACTTGAACCTGGTCTCGTTGCCAATAACTCGTCGGCGTGCAGGACGCGGGCGAACAG
TACCTCGGCATCAACCGCGTCCGACCTGAATTGGCAGCAAGCGCGCTGCTGGCGGATGGTGAATCTAACAGCAGC
CTCTTCCCGTACACCAACCCGACGGCGCGCTGCCCGGGCGGAACGTTGCTCGACACCATGATGCAAAACCTTC
CCGGGAGGGCGGATGC (SEQ ID NO. 320)

Clone Rv274

:::::::Rv274SP6.seq:::::::

TTCCGAATTCTGGTCCNGGTATGACCTCATGGAAAGAAGAAGCGGCCGCCCGTGCACGGCGAATGA
AAACCCCTACCCAGGCCATTGAACGCCGACAAGACGGTGGAGCAGGTGCAAGACGTCCTGGACGGTCTGGTAAGA

CCATGGCCGAGCTGAACAGCTCGCTGTACAGCTGAACAGCACCGTGGAGCGCTGGAGGACGGTCTGGACCACATCTCG
AAGGTACCCCTGCACAGCCTGGACGATCTCGCAGAACGGCTACGTGTGGTCAGGCCGTGGAAAGCCATCGTCGATC
GGATCGACTACATCGTGGACCTCGCGAAACGGTATGTACCGCTGTGGTC (SEQ ID NO. 321)

:::::::::::Rv274T7.seq:::::::::::
NCTCGATCTGGGGTACGTTGATGAGGCTGCTGACCAACAACCCGGCAAGCGGGTGGGACTGGATGGATACGGATT
GCACATCATCGAGCGCGTGCCTGCCGGTGCAGGGCAACCGGAAAGAACATCCGTTACCTGATGACCAAGCGTAC
AATTGGGGCACGACTTGGCTGGGTTGGACGATTTCACGAATCCGTCATCTGCCGGAGAATTGGCGGTGCCTTGT
GAAGGTGGCGCCGGGTGCCGGATCTGCCGTCGCTGGATCGTCTGGTGTGCGGCTGGCGATTGTCGCCAGCAGCTGGC
ACGAAAGATCTGCGACGCGCTGGACGGCGCCCGAAGTGGCGCCGGGTGTGGCCTCGATGACCGACTGTGGT
CGGGTGTCCCGCGATCGATAT (SEQ ID NO. 322)

Clone Rv275

:::::::::::Rv275SP6.seq:::::::::::
TCATCCCACCAAAACGCGAGCTAGGTCGGCATCCGGAAAGCATCGCACCCGTGGCGCCAGCGCGCTGCCGGCAG
GCCGATTAGGCGGGCATATTATCCCGCCGCGCTCCCGCTCCGAGTACGGCGCCCGAATGGCGTCACCGCTGGTA
ACCGCTCTGCGCGCTGGCGGGCTGCCGGATCAGGTGGTAGATGCCNACAAAGCTGCCGATCGGTACATCAC
CAACGGTGACAGCAGCGGTTGTGCAACCAAGCGCAACGCCACCCGGTCTCCGGGTCTGTCCAAACCGATCGACCGCC
CAAGCCCACATGAACAAACCCCGGATCACGTTGCCGATCGGATACCGTGA (SEQ ID NO. 323)

:::::::::::Rv275T7.seq:::::::::::
TTGGCGGGTTGGCCCAGCAGCCCGCCGGTACGGCGACGATGCTGGGTGCGGCCCTGCGCCACCGCGGCTTGC
ATGCTGGTTGGCTGTTGGACGATCCGAAATAGTCCACCGGATCTGGTATTGCGGGCTACCCGCGATTAC
CCCGCGGGCTCGACGAGTTTGCGCTGGACTACCCGCGTGGCAATCTGCTGAACCTCGCGCCGGTGGTGCCTGG
ATGTCGAGCGCCGTTACCTACGTTGACCTGATGGATCGGGGATGCCGACCGTGCCCGCGATGTGATGTGCCGG
AGCCGGTCCGGTTGCCACGCAAAGGCATGCTTGTGCGGTTCCGACCATCGGTACCGGGACACGGCGCTGTATTGCC
GGTCGCTGCCGAGTTGTCGCGCAACTGACGCNGGCCAGCGGTGCTCGTTCANCCGGAGGTTCCGGTGACG
ATGATCGTGTGGTCTCCCT (SEQ ID NO. 324)

Clone Rv276

:::::::::::Rv276SP6.seq:::::::::::
GTAGGAGAGAACAAAGACCGTCGATAGGACACGTGTTACGCCGGTAGCTGTCAATTGGTATGGGTGCGCTGCCGGGG
GGCATCTACTCACCGATCGGTTGTGGAGGCCGTTGCTGCCGGGCAACATCTGGTACCGAGATCCCGCCGACCGC
TGGGACATCTACGAGTACTACGACCCGAACCCGGCGTCCGGGACGCAACCGACTGAAATGGGCGCGTACCTCGAT
AACGTCGGCGACTTGTGATCCCGAGTTCTCGGGATCGGGAGAAAGAAACGATAGCGATCGCAGCACCGCTTG
TTGCTGGAAACCTCTGGGAAGCCATGGAACACGGCGGGCTAACACCGAACCATATGCCCTCCGACANGGGTTTCGT
GGGGTT (SEQ ID NO. 325)

:::::::::::Rv276T7.seq:::::::::::
CGAACTGAGCCCATAGAAAGGCAGCGACTAATTGCGTGGCAAATAGGAAGACCCTTGTCCCTGCCACGTATATTGT
CGACCTCGTTGCGAAGGAAGCGGGCTGCCATTGGTGCCTTCCCTGGAGAATCTGCCCAGCAGGAAGTCTTAT
GAGTTGACAAGCAGGGGCGCCGCTTCGCCGGAAATCACATTGCGTCAATGAGAGCGCTCCAGGTGCG
GATGCTGCCAGCGCCGCCACGATACGACGCCATCGCGCCTGGGCCGTCTCGACCACGCCAGGTTGTGGT
CGTGGCGATCTCATGATCGCGTCCATCTCGCAGGCCACCCGGCATAGTGAACGGGACCATGGCCTCGGTTGCGGG
TGAA (SEQ ID NO. 326)

Clone Rv277

:::::::::::Rv277SP6.seq:::::::::::
CTTAGACGCCACCTCCGGGGCAGCTCCACGGGTGGATAAGTACGGCCGGATGTGGCCGCAATGGGAAGTTGTTGCC
CGCTGACTGTCGGGTTAACGCCGATTCCACACATCCCTGCGAAAGGCCGTTGGGTT (SEQ ID NO. 327)

:::::::::::Rv277T7.seq:::::::::::
GATCGCGATCGTGTGGCCATCCGGCTTGGCGTCACCCCGTAAGGCAGACAGATGGTTCGCGGCACGGTCAA
CCTGCCACACGCACTGGTAAGACTGCCGCGTCCGGTATTGCGGGTTGGTAAAGGCCGATGCTGCCGTTGCCGCG
GGGGCTGATGTCGCGATCGACGATCTGATCGAGAGGATCAGGGCGCTGGCTGGAATTGCGATGCCGCGATCGCGAT
ACCGGATT (SEQ ID NO. 328)

Clone Rv278

:::::::::::Rv278SP6.seq:::::::::::

AGCTTACGCCGTTCGCTTCNGATTGGGACGCCGCATCGAAAGCGCAGTTGGAAGCGCGCCGGCTGGTCAG
 CTGCTCAAGCAGCCGCAATCCCAGCCATGCCGTTGAGGAGCAAGTGGTTCGATCTCCTGGCACCGGGTCA
 CTGGACTCGGTGCCGTCAAGGATGTCGGCGGTTGAAACCGAATTACTGGACCACATGCGGGC (SEQ ID NO. 329)

:::::::::::Rv278T7.seq:::::::::::

CGACGGGACCTCGTCGCATCTTCATAGCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTATAAGGTGGC
 GAAGCGCTCGGCATTGGTCATCGGGATATGCCGCTGGGACGGTCAGATGCCCTCGGGTCCNGGCAGCACTCCTCAGG
 CTTCGTCGGGGTGGTCGCCACCGCATGGGCACATCGCATTACCAGGTCGCGCAATCACCAGCACGTANACGGTT
 CCTTCTTAAGCAACACCGAAATTTCAGGACCCGAATGCTCCGGAAAACATGTCACGGTAAGTCCGGTATTCCGGGT
 ACCGGTTGAGCATTGA (SEQ ID NO. 330)

Clone Rv279

:::::::::::Rv279SP6.seq:::::::::::

CGGCATCGGTTGGGCTGTCACCAGCAGTTGGTAGTTCTCACTACTGTTGTTCGAGCGTCGAGCCGCCGCGTGTGTC
 GAGGTCGCCGGACCGTACCCGCCAGGCCAGGGTCCAGGTCAGTCCACGCGNCTGTGGTCGGCTAACCGCTTA
 TCTTCATCGAGACNATGCCAGCTTCATCGTGTGGCGATCTGTCCGAGGGCACCTGAACCGGGCTGCGANTAC
 AGCCACCGGATCGTGTGCGCCCTTCGCGTCGACCATCGTCGATACCGCAGGCACTTGGCCCTCGAGCAGCTGGCCGAT
 CGTTGGCAACGACCTCAGAGGACGATTGGACATCAGCCCTAGCCCGCTCGC (SEQ ID NO. 331)

:::::::::::Rv279T7.seq:::::::::::

CCGTCGANGCCGCCACTTGGCTTGACCGACACCAACATGGCTGAGGGTGTCAACAAGACCGTGGCCGACGGGCTG
 AACATCACCAGGCGCATGAGGCCACGCCACCGAGTTCATCATGTTGATCGCCGAAAACCATTGGCGGGTAGCGGAA
 GAACGGTCGAGGGTGTCTACACCGAGTATTGAAAGTCGAAAGGCCAACCGCTGCTCAACGGCGTCAACATCATTTCG
 ACGGGTTTCTGCGAGGGAGGATGCCACGATGAACTGGATCCAGGTGCTGTTGATCGCGTCGATCATGGGTTGCTGTT
 CTACCTGTTGGCTCGCGCCGAAGCGCGCGGTCCGCTGGTCAAGGTGGGATGTCGCTGCTCCGGCA (SEQ ID NO. 332)

Clone Rv27

:::::::::::Rv27SP6.seq:::::::::::

TTACACGNCTGCTTCCGGCTCGTATGTTGAGCGGATAACAATTACACAGGAAACAGCTATGAC
 CATGATTACGCCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTTTGAGCGTCGCGGGGAGCTTCGCCGG
 CAATTCTACTAGCGAGAAGTCTGGCCCGATNCGGATCTGACCGAAGTCGCTGCGGTGCAAGCCACCCCTATTGGCGAT
 GGCGCCGACNATGGCGCTGGACCGATCTGTGCGCTTGCCGACGGNACGCGGTANGGGTCAAGTCCGGTCAACN
 CTTGGGCTTTGCGGACGGTCCCACCGCTGGTCGCGGTGCGCCCGGGAAAGCGGGGGTGGGTGCCATCAGGAATG
 CCTCACCGCCGCGGCACGTGACGGCACTGCGCCGGCGATGTCNGCCATCGGGACATCATGCTCGCTTCAACTCCT
 CGACC (SEQ ID NO. 333)

:::::::::::Rv27T7.seq:::::::::::

CAGGCATGCAAGCTTGTACACCAAGTGGTGCACCGAGGCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCA
 GGTGCCACCACGCTGGTCAGTCGCGCTTCAGCTCGCTGCCGCTGCAAGCAGCCAGTCCGGGAAATAGCTGCCCTG
 GCGCAGCTTGGGATCGCACGTCGATGGTGCAGGGTGTGCAAATCACGGTGGCGGTAGCGTTGCGCTGATT
 GGACCGCTCATCGCTCGCTCGCGTAGCCGCCACAGGGCGTCGGCTCAGCCCCATCAAGGGCG (SEQ ID NO. 334)

Clone Rv280

:::::::::::Rv280SP6.seq:::::::::::

AGCTTAGCCAGTTTTCTACTCTGGCCCACACCCACAGTGCTCGACGGTACGGTCACCCATGATGGCCATCCAGT
 TGGCATCGGTGAGCTGATAATGCCAGCTGGTTGCCAACCCGGTAGCGATCTTGGCGCCTGCTGTTGTCAGTGA
 TACCTATCGAGCAAGACAGCCCGGTTGCGACAAGATGACTTTCGGATCTTCGGCAGTCGATGGGTTGCGTGG
 GAGTCCCAGGGGCCACCGCGAGGTAAGCCTCGTCCAGCCACACCTCGACCGGGTATCCAGGTCGCGCAATAACG
 CCACCACTCCTCGGACGCCGCGTTGAGGCGCTGGGTTGACGGCAAGAAGTGGCCTCAGGGCAGTCGCGCG
 TCCCAACGGCAGTCGCGGCCACACCGTAGGCGGGGCTC (SEQ ID NO. 335)

:::::::::::Rv280T7.seq:::::::::::

CCGGCGGAACCTAGACGTGCTGGTGGCGCATGGCACCGCGGGCAGCAAAGCGCACTTCTCCGGGACGACAGCAA
 GCGACCGCTAGACAAGAGGGGCTGCGCAGGCGAGAAGCGTTGGTACCAACAGCTGCTGGCGTTGGCGCCACCGATGT
 TTATGCCGCCGACCGGGTGCCTGCCACACGACGATGGAGCCACTCGCCGCGGAACGAGTCGACCATACACAACGA
 GCCCACCCCTGACCGAAGAGTCCTACGCCAACACCCAAACCGCGGCCACACCGAGTGGCTGCAAGATCGTCAGCGAAGT

AGGCACACCCGTGATCTGCACGCAGGGCAAGGTCAATTCCGATCTGATCACGTGGTGGTGCAGCGCGACCGTGTGCC
 CCCGACAGTCCCGCAATCGCAAAGGCAGCACGTTGGTGT (SEQ ID NO. 336)

Clone Rv281

:::::::::::Rv281SP6.seq:::::::::::
 GTATGGTCAGCTGTCCATCCGGCGCTGCGCCGAGCTGCCAGATCTGTCAGCCGTAACCGGGTGCAGGGATCCACG
 CGTGGGGTTGTCTAC (SEQ ID NO. 337)

:::::::::::Rv281T7.seq:::::::::::

CCGACTTTCCGGGGTACCCGCTCAACTTGTGTCNACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCA
 ACTTCATCCTGACGCCGGAAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACT
 ACATCATTCGACGGAGAACCTGCCGCTGCTAGAGCCACTGGATCGGTCGGGATCGTGGGGACCCACTGGCGAAC
 TGGTTCAAACAAACTTGAAGGTGATTGTTAACCTGGCTACCGCAGCCGGCTATGTTATTGACCTCGCCGCCAA
 TGTTGCACTCCGTCGGTTGTTCCAGAANGTCAGCCG (SEQ ID NO. 338)

Clone Rv282

:::::::::::Rv282SP6.seq:::::::::::
 GCACCGATGTCGGCGAGCACTCGTCAACTCCAGGGGTGCCCGACCAAGTATTGACGAGTATTCCGTCGGGCC
 GCCGCCGCCGTGCGCGCAGGTGGTACCTGGCGGGCTGGGACTCGCGCGTACCGGCTGCC (SEQ ID NO. 339)

:::::::::::Rv282T7.seq:::::::::::

TGCACCCAACCTACTGAGCATGCTAACGCTGGTGTGCGGGTCTTGTTCGGCGTGTGGCAGGGCACACGCTCGGG
 CGTAGCTGGGAGAGGCCCGGTCAAGGCCGGAGAGCAGTGCCTAGTCCGCCAGCTGACCGACTTCGATGAGAACGC
 GCTTCTGCCGTATTGAACTGGCGTGTGACGGTCGCTGAGCAGCGCTGCCAGTGCAGGGCTGATTCTTCATCG
 AGCCAGGACGCCATTGTCGGCCGC (SEQ ID NO. 340)

Clone Rv283

:::::::::::Rv283SP6.seq:::::::::::
 AGCTTACGGCCGGTGCACCGACGAGTGGTTCATGACACCACAAACCGTCAACGCCACTACAAACCCGGGATGAACG
 AAATCGTCTTCCCGCAGCGATTTCAGCCACCATTTTCGATCCGCAGGCCAGGAGCCAAACTACGGCGGGAT
 CGGGCGCGTGATCGGGCACGATGATCGGGCACGGTTTCGACGATAGGGGCCAAATACGANGGCAGC
 CNATTGGTGGATCGA (SEQ ID NO. 341)

:::::::::::Rv283T7.seq:::::::::::

ATGTCGTACGTCAACCAATCGCAGGGACCAATCATGCCGCCAGGGCGCCAACCCAAATGGTGGCGCGAAGCG
 CAGCTCGATCGCAGCGGGAGGTGCCGCCGCCAGTTGATTACGAACAGGTGAGGTCAAGGGCAGGATAGTG
 ACGAACGCAAGACCTATATCTGCCGTGGAGTAAGAATCGAGTAGCCGGTCAACCGGAAGCGAAAGTGTCCCG
 TGTTGATGAGCGTCGCCGGTTGTCGGCGGGTGGC (SEQ ID NO. 342)

Clone Rv284

:::::::::::Rv284SP6.seq:::::::::::
 AGCTCACCAAGCGTGCGATGCTGGTGCNAACCTCTACTATGCGCAATTGCCGACACGGTGGCATCAACACG
 GGCAGATAAGGTGGACATCGCTGGGTGACGTCGGCTGGTGCCTGCCATCCGCCAACCGCGTGGTGCATC
 GGATTCTCGTGGCCCGCAAGACAATCGGATGCAAAGCCGGCAGCAATTGCCACCGACACCATTCTGCC
 AACCTGGAAATCGAACCCCGGGTTCGGAGCGTTGAAACCCACGGTTCCCTGCCGTTGGCGCAGAACACTACGCC
 TACCAAATCTATGACCGTTCGTC (SEQ ID NO. 343)

:::::::::::Rv284T7.seq:::::::::::

CTGCCCGGGTGGCGGTCAAGCGCTGGCAAGTCACCGCACCGCGTCCGGTTCATCGGCAGGCTCCCCGAAAAGGG
 CTGGCAACAGAAGGTGATCAATGAGCTCCCGCAGACCTCGCCGATCTGGGACCGACATACGTGAAGTTCGGCCAGAT
 CATCGCGTCCAGCCGGGAGCATTGGTGAGTCGCTGCGGGGAATTCCGCCGCTGCTGCCGACCCGGTGC
 CAAAAACCGACGAGGTGCAAGCTTCGTCAGGAACTCGCGACGAGGCCGGGGCTGTTCGCCTCCTCGAGG
 AAGAACCGTTCGCGTCTGCCCATGCCCAAGTGCAGTACCGCAGCGCAGCGGAAGAAGTGTGGTCAAGATC
 CACGGCCGGGCATCCGCCGCCGCTT (SEQ ID NO. 344)

Clone Rv285

:::::::::::Rv285SP6.seq:::::::::::

GATCGTGCCGGCCCCCGGGCAGTAGCAGATCAGCTCGAAATCGCGCAACCAGTCAGTCGATTCATACG
 GGCGCCGTCAATCAACTCTCGAACATCGGATCGGACCGGAAACCGGGAGCCGCTCAGCCAGCGCAACCAGCAC
 CGGGATCGGATGAATCATCAATATTATCAAGTGATTCTGTGATGGCATCGAGCTCGGTGATCTGGTCTCGGGGCA
 GCTCGCCGTGGCGACGTCGATCCGGCGGAGCGCATAGACCGAAATAGTGGCCTCGCTTTCGCGGGCA
 AGAGTCGGATGCCGTAAATATANGTTCTGGCGGCGTGCCTGATCNACTCGGTGATTCGATACGCCGTTCATCTC
 GGTGATGCCGTCTC (SEQ ID NO. 345)

:::::::Rv285T7.seq:::::::
 GGTGGCGCAATGACCGAAACCCACCCCCAGCCCCGCAAACCCCCGGCGGGCCCCGGCACAATCGTTCGTGTG
 GAGCGGCCATCCAGACCGTTGGCGCGTAAAGGAGGCCGTGTTACGAGTGGCGCTGGTGGCCGACCGCAAGTTC
 GACCTCAACGGCCGAGCTGGAGGACTACTTCCAAACAAGGTGACCCAGCAGTTGATCAAGGACCCCTGGTCACC
 GTGGATGGGTGGAAAGTTGACATCTTGCCCCACCTGGCGGGCGGCGCCGTGGGTATGGCCGGCGCTGCG
 CCTGGGTATCGCCGGGATTGATTCTGATCGCCGGATGACCGGGCGCTGAATAANGCCGGTTCTGACCGT
 GATCCACCGCCACCGAACGAAA (SEQ ID NO. 346)

Clone Rv286

:::::::Rv286SP6.seq:::::::
 CACAATAGATTACTCAAGCTTCGAACCGAGCGCCCTTACGTATCCCGCTGAGACCTTGACCCCTAGGGCCGAAGT
 GACTCGCTGCTGCTATGCCGACACCGATTCCAGACGCTGCTGTTACAGACGGCCGGCCGGTGGCCACCATCAC
 GCTCAACCGCCGGAACAGCTAACACCATCGTCCCGCCCATGCCGACGAGATCGAGGCCGCTATGGGTTGGCGA
 GCGCGACCAGGACATCAAGGTATCGTGTGCGGGTGCCTCTCCGGGTTACAACCTCGGGCG
 GTTCAACATTGGGGCAT (SEQ ID NO. 347)

:::::::Rv286T7.seq:::::::
 TCAGGACGCTTATGGTGGCAGATGGTGCCTGGCGTCAATCGCGAGCGCATGAGCTACCGGTTCGGAACAA
 CGTATCGAAGAACGTCGACTGCTGGCAGATGGTATCTCGATGTTGTTGTAATTGATCCAACTCTAACTGTGCT
 ATCGATCAGCGTGAATATCGAGATATTGCGAATGCGATGACAGGCCGATTCGGTTATCGCTTACGCTTCCGG
 GTTCGATTGCTGTGACTGCCGAAACGCCGATATGATTGTTGAAACCGTATCTAACGCAATTATTGATGTGTT
 AGGCGGAGCTGCCGTTTGTGCTGCGGTATTGATCGGGTGGGGTGTGCTATGCCCTCTGCTCCCAT
 (SEQ ID NO. 348)

Clone Rv287

:::::::Rv287SP6.seq:::::::
 CGCAGCTGTCGCCGATCTGGTCCGGAATACCTAGCTCCAGGTTCTGAGTGGAGATGAGTGCAGGCATCGAAGTGTG
 CAATGTAACCCAGGATGTCAGGTGCCAGGCCGCTGGCGAGGATCTGGGACCGCCGATGACTGGTCGAAGTCGG
 CGAACGGGGAGCACGCTGGCGTGTGGTC (SEQ ID NO. 349)

:::::::Rv287T7.seq:::::::
 GTAGTTGTTCATCCAAACACAGTGGTACCGGCTCAAGCGGATCACCGACTTCACCGGGCGCGATCCCACCCAGCC
 ACGCGATGCCCTATGTCCTCGGGTGGCGGCCACCGTGGGTCAACTCAACTATCGACGCCGACTGAAGCATCGACAG
 CAATGCCGTGTCATAGATTCCCTGCCGGTCAGAGGGGGTCCAGCAGGGGCCCCGAAAAGATACCAGGGGCCGTC
 GGACCGA (SEQ ID NO. 350)

Clone Rv288

:::::::Rv288SP6.seq:::::::
 TCCGCTCGCTCTCCGAGAGGTTGAGTGCCAAACGCTCTGGCGATGCCGAAGCGGGCCCGGTGATGACGGCAGCCT
 GCCTCGAATGAGCTATTGACTACTCCCGTGGTGTCCCTGCGATTGGTGGAGGTGGCCGCGAGCCTGCCCC
 AGGTGGCGATCGGTCTCGGGCTTCGGGAGCAGACTGACCTGCGAGATGGAAGTGTGCCCCATGCCGCAACCG
 CGATGCTCGATGCTTGTGTTGCAAGCGGGCGAGGGGTTGATCTTGCCGCTAACACNGATGGATCGTCC
 CGGGTCTGCATGACGAATGGCG (SEQ ID NO. 351)

:::::::Rv288T7.seq:::::::
 ATGGGAGGCCACCGATTACCATCTTGACACACCGATTCCGGCTATTGATGTCACGTTGGTCCGCAACCGCGCT
 GTGGCTGCTGGCCAAGGCGAGGGGATACCGAAGTCAGTGCCTCGCGAGCCTGCGATCCGAAATGGAATGGCG
 CGAGGATGGTGGCTCGTGCAGACCGTCACCGAGCTGCGGTCACCGTGCACGGCAGCTTACACCCGACCAA
 GATCCGAAAGCTGCAAGCTCCAGCACCGATCCGACGTATCACCGCTGCCGCCCCGACGTTCTTGAACCTATTG
 AGCTGGAATCGGCCGTCGGTTGCTGGATTGCGNTAAGAACTGGCCT (SEQ ID NO. 352)

Clone Rv289

:::::::Rv289SP6.seq:::::::
 GCTTTCGCGCTTCTCCGAGAGGTTGGAGTGCCAACGCTCTGCCGATGCCGAGCCGGCCGGTGTGATGACGGCGACC
 TTGCCTTCGAATGAGCTCATTTGACTACTCCCGTGGTTGCTCCCTGCATTTGGTGGAGGTGGCCCGCAGCCTTGC
 CGAGGTCGGCGATCGCGTCCGGGCTTCGGGGAGCAAACCTGCAGATGGAAGTCTGAGTGGCCACATGCCCGAACC
 GGCGATGCTCGATGCTGTTTCAAGCGGGCGAGGGGTTCGATCTTGTCCCGTCAACCGCAGATCGGATCGTC
 CGCGGGTCTGCATGAAGAAT (SEQ ID NO. 353)

:::::::Rv289T7.seq:::::::
 CTCACCGAGCCACGCCGTACCTTCAACGAAAGACCTCACCTGCCGATCGAAATGGAATCGGCCGTGACGAAATTG
 GCGCAGCGAAACACTCAACGAGGTGGTGGCTTCGTGCGAACCGTCACCCGAGTCGCCGTACCGTGCACGGCGAC
 GTTCTACACCCGACCAACATCCGAAAGCTGCAAGCTCCAGCACCAGTCACCGTCACTACCCGCTGCCGCCGGCA
 CGTTCTGACCTATTGAGCTGGATGCCCGTCCGGTTGCTGGAGTGCAGGTTAGAAACTGGCTAGAACCGGGCG
 GCACACCGCACCTGGCGGGGN (SEQ ID NO. 354)

Clone Rv28

:::::::Rv28SP6.seq:::::::
 TGCTTCCGGCTCGTATGTTGTTGGAATTGAGCGGATAACAATTACACAGGAAACAGCTATGACCATGATTACG
 CCAAGCTATTTAGGTGACACTATAGAAACTCAAGCTTGTGCGCCGAAACCGAGCGTGGACCGCCAGCCACC
 ACNCGGGTGGGGCGCCGGCCGGTGCAGCCANGCTGCTCCGCTCGGTGATGGCACGCCACCGCAGACACCACCGGC
 TGCCTACGTCGAGCCATACCGGGCGGAGCTACATCGGCTCGCCGCCCCAGTGTTCGGGCCCTCTTCGAAGTCAAG
 TCGATACCGATTGCGCATCCGNGCCGCA (SEQ ID NO. 355)

:::::::Rv28T7.seq:::::::
 CAGGCATGCAAGCTTACGTCGCTACGGCTCGGTACGCTTCGGTCGAGTGTGCGAGTGATAGATGACGACCGGGAC
 CTCGCTGCATCTTCCATAGCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGTGGAGGTCGGCGAGCGCTC
 GGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGAACCTCGGGTCCGGCCAGCACTCCGAGGCTTCG
 GTGGTCGCGACGCGCATGGCCACC (SEQ ID NO. 356)

Clone Rv290

:::::::Rv290SP6.seq:::::::
 GCTTGTCTATCGTCCCAGGTCCGGCAGGTCCGGCAGTCAGGTCGAAGGCCAGTCGGTCTCCTCTCCACTACGCCAAGA
 ACTGGCGACGGTGTAGTCAGACGACCGGAAACTGGTGGCGCCCTAGGCGAGCGACCGCCTCACAAACGGCGGTGA
 CCGCGTTCTGGTGTGCACCATCGAGCCGTGCCAGCCGGCGCGTGCCTCAGCCGATCCACTGGATGCCCTCT
 CGGGTTTCAATCAGGTACAGGCAGTTCGCCACCATCGTGCCTGGGACGGTTAGCGAGAAACGCCGACTTCAC
 GATTGCCCTCGGTGATGCCGTCGAAACAGATGGGCT (SEQ ID NO. 357)

:::::::Rv290T7.seq:::::::
 GCGCGCCATGTTGAGGTTGTCGACGGTGACGACGGTGAAACCAACTGTTGACCTGTCGCCACACACCGTGTGGAT
 CGGGCAGCGGACCCGACAATCGATGGCGCGCACATCGCGTTGCCAGGTGATTGCTAATCCGGTGGGGTCAAGTT
 GGGCCCCAACATGACCCCGAACCTGGCCGTGGAGTACGTCGAGCGGCTCGACCCGACAATAAGCCGGCCGGCTGAC
 TTGGTGAGCAGGATGGGCAACCACAAGGTCCGCGATCTGTTGCCACCGATCGTGGAGAACGTCATGCCACCGGGCAT
 CAGGTCACTGGC (SEQ ID NO. 358)

Clone Rv291

:::::::Rv291SP6.seq:::::::
 TTGCCTTCCATGCCGAGCAAGGTGACTCAGCGATGACGAATTGTTCTTCTCGCGGGGTGTTGCTGCTGGTTGCC
 TATGAGAGCACTGCTCATATGATTAGCACATTGTTCTGACGCTGGCCACTATCCAGATCAGCTGACACTCCTGCG
 CAGCAACCAGACCTGATCCGCCGGCATCGAGGA (SEQ ID NO. 359)

:::::::Rv291T7.seq:::::::
 CGACGCTGGGCCAACCTGCGACCAACAGGTCTGGTATGGCAGGACATGCCGGGTTGAGCGGGGCCAACACCG
 (SEQ ID NO. 360)

Clone Rv292

:::::::Rv292SP6.seq:::::::
 TAACGACTCGGGTCCAGCGACCGCGCAACACNAACGGCCGACNACTGGGCCAGGGTGCAGGGCTCCCTACAAAC
 AGGATCCGTTGCCCTGCGAACGACAGGCTCCGGTGCAGGGCTGCTCCAGCGTCCGGTCCCGGTG

CCGGCGACGCTTGTTCCTCCATACTCGCCCCATACTCGAGGCAGCCGTACCCGAGGCAACCTCCAAAAATGC
AATCCCCAAAATGCAATGCGTCAGCTATTCTCACACCGACCGCTAGTTGCGGATCANAATCCGTTGGCGCGGA

(SEQ ID NO. 361)

:::::::::::Rv292T7.seq:::::::::::
CNTGGCGGTGGGTGCGGTGCGAACACGACCAACTTCTTGCCTCGGTGATCTCGACACCAGGCCGAGGCCACC
ACCATGCGCGTAGATCGCGATCAGCGCGTCGGCTATCGCCTGGGTGCCGCCACCGGAATCGGCCAGCCGACCGA
ATGGGCCAGCGTTGCCATCATCAGTCCGGCGCCGCCGACACCCAGTGACGGCAACGGTGAATCNCGTGGCGAAC
GCCGGTGAACAACGCGCGGCCATCTCGCCGCCAGCGACCGCCAGGCAGGGTGCCTGGGCCAGCATCCGAGCCC
GAGACNCAGGACCGANCCCAGTG (SEQ ID NO. 362)

Clone Rv293

:::::::::::Rv293SP6.seq:::::::::::
GCTTTTNGATCGCAGCGAGTCGTACCCCGCCTGGTACCTTCGTGGATATGCCGCCCTGGTCAAGGGGGCGTCCGA
GGGAGCCGGCTGGTAACAAGTTCCCTGGCTCATATCCGCAATGCNACGCCATTGTCAGGTGGTGCGGGTGTTCTCGT
CAACAAACNACTTGACTCATGTCACCGGACGGGTGATCCCCANTCCGACATTGAGGTGTCGANAACCGAGCTGATCCT
GGCANATCTGAAACCCCTGGAGCGGGCACGGGCCGGCTGGAGAAGGAANC CGCACCACAAAGGCGCGAACGCCGGT
CTACGACGCGGCACTGCGTGCCTCAGCAGGTGCTCGACGCCGCAANACGCTGTTGCCCGGGGGTGGATGCCG

(SEQ ID NO. 363)

:::::::::::Rv293T7.seq:::::::::::

GTCGTACGCCATTNGCTGGTGTGCGCATACCAAGTACGACGCCGGCACCTGACGCCGGCCGACCAGTCGGTG
GCCATGCCATCGTCTGCCACCGGTCAACCGACCGCACCTCTCCTGGCCGACGTAGTGCGCCACCCGCCCGCTTG
CGTCCCACCNATCCGGTCAACATGAGCAGCGCAACACCAGCGGGTACATGACATCGCTGTGGAACCAAGTGCAGATT
CCGCCGCCATGATGATCATGACCGTCTCCGGATTGGTGCCTGGTGGGGGCAAATTCCCTGGCAAACCGGATTG
CTGCGCGGCCGGCACACCGGTGATCGACTCCTGCGCAGGCCGGGGTGGTCTGCTGGGTTGGTGCCTGGTACCGG

(SEQ ID NO. 364)

Clone Rv294

:::::::::::Rv294SP6.seq:::::::::::
GCGAGGCAGGTATCGCTCCCGTCGTACCGCGACCGAGCCAGGAGAAGCTCGTTTCCCAAGTGTGCTGGGGATTCTC
ACGCTGCTGCTGANTGCGTGCANACCGCTTCCCGTTCCGGTTACAACCGAGCCGGGGTACGATCGCAGCGTG
AAANTGGTGTCTCCATGGACTTGGGGATGTGCGCTGACCCGGTTACCTACNACTCCAAGCTGGCGCGTCTCGTCCG
CAGGTGTTGCTGCGATAGCGGGAGGCCGGATCCGAAATGACGGATTCCATGCCAACGCTCCGAGTTGCGATGCC
ATCGAATACNAATTGATCACCCA (SEQ ID NO. 365)

:::::::::::Rv294T7.seq:::::::::::

TGGGTCTTGCAGCCGAGCCAGCGAACGCTAGCGTGGCCGTGTTCTGGCTTCGGATCTATCCTCGTACATGAC
CGGCACCGTGTGGACGTGACTGGCGCCGGTTCATATGACACCGAGATCATTGCCACGGTACGGAATTCGTCAAGA
AGGAAATCTTCCCNATGCAACGGCCCTCGAACGTTGCAACAGCTACCCGAAGAAATCGTCGATCGCTGGTGT
TTGGCTGCTGGTGCCTGGTCAAGGGTATCGACACCACCGAGTTACCTCTCGGGCTGCCGGCATTGAGCTG
GCGGTGCGCGTGCCTGGCAGCACCGTCAAAAGTACTTGANGATGGTCAAACGTCGGACGAACCGCACCACGTCGCG
GAACGG (SEQ ID NO. 366)

Clone Rv295

:::::::::::Rv295SP6.seq:::::::::::
TAGATGCCAAGCTGCCNTTANAGACCTCGTCAACGGACGGACCGTCAAGGTGGCAATCCGGCTTG
GCGTCNACCGCGTAAGGCAGACCAAGATGGTTCGCGGACGGTCAACCTGCCACACGGCACTGGTAAGACTGCCCGCG
TCGCGGTATTCGCGGTTGGTAAAAGGCCGATGCTGCCGTTGCCGGGGCGGATGTTGCGGAGTGACGATCTGA
TCGAGAGGATTAGGGCGGCTGGCTGGA (SEQ ID NO. 367)

:::::::::::Rv295T7.seq:::::::::::

TCTCCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTCGCTTAG
CGCCGGATTCCACACATCCCTGCGAAAAGTCGTTGGGTGCAATGATGTTAGCGCTTCTCCCCATCGAGATACTG
AGCAACGCAATCCGTGCGGTACGGTTGGTCTGACTCGATGTCGCGACCTTGGCGTTGACACCACCTTGTGATTG
CGCGAAAGTCGATCATCCGTAAGCGCGCTATGACCGCCCTTGTGCCGGTNGTAATCCGGCC

(SEQ ID NO. 368)

Clone Rv296

:::::::Rv296SP6.seq:::::::
 GCCCGGTTGATCGGCATGGCGCAGTCGTCGTTACCGGAGGCGCTGGCCGCCTAATCGCGTCGGCGCCGAC
 AAGATGTGGGATATCCGCAATCGGGCGCTCATCCCTCGGGCGCTCCCCCGCTCGAGCCTTCGTCGACGCAATC
 GAGGCAAGTCACGACGGATGAGGGGCAGCAGTGAATTACAGCGAGGTCGAGCTGTGAGTCGCGCTCATCAACTGT
 TCGCGGAAACAGTCGGCGACCGGGGTTGGATCGGGCACACCCCTACGGGGATCTGCTCTCGGCTGCCGAC
 CTGAATGTNGGTGCGGGCANCGCCGTATCNACTCCGTGGAACACAGCCGGGC (SEQ ID NO. 369)

:::::::Rv296T7.seq:::::::
 CTCGGCGTGGATATCGGTGAGCCGGCCGGTGAANGTCGGCTCCTAACGTCACAGCTCATAGCGATC
 CAACCGTANGCAACCGCTTCAGCAGTACAAACCGCCGGCGAACACTCGCAGTTGAACCGCAGCTGCCCTGGGTCAAG
 CATGCCCTCGCCGGTTGTCAGCGAAGGCCGCGAACAGGTAAATGCGTCACAGGCTCGTAGAAACGCCAGAACAC
 GGCCACGAACAGCCAGTTCAAGCACCAGGGTAGAACCGCAGATCGAAGACGAAAAAAACCAATGTCATAGCGAATT
 CGGGTCCACGATGCCAAGGTGCCCCCGTGTACAACAACTGAACCTTCACCCA (SEQ ID NO. 370)

Clone Rv29

:::::::Rv29SP6.seq:::::::
 TCCGGCTCGTATGTTGTTGGAATTGTGAGCGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCAA
 GCTATTAGGTGACACTATAGAATACTCAAGCTTCACGTCGGTACGGCTCGGTACGCTTCGTCAGTGTGCGAGT
 GATAGATGACGACCGGGACCTCGTCGGCATCTTCATAGCCCCCACACCTTCAGTTGCTCACCGGAATCCAACCGGT
 AGAAGGTGGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGTCGGGACGGTCAGAGCCCTGGGTCCGGCAGCA
 CTCCGAGGCTTCGTCGGGTGGTCGCGACGCGCATGGCCACCATCGCATTACCAAGGTCTGCGCAATCACCAGCA
 CGTAGACGGTTCTTCTAAGCAACACCGAAGTTCAAGGACCGAATGCTCCGGAAACATGTC (SEQ ID NO. 371)

:::::::Rv29T7.seq:::::::
 CAGGCATGCAAGCTTGATGCCGCCAAACCGAGCGTAGGCACGCCGCCAGCCACCGCCGGGTGGCGCCGGGCC
 CGGGCCGCCAGGCTGCTCCGCTCGGTATGGCACGCCACCGCGACACCACCCGGCTGCGTACGTCGAGCCATACCGG
 GCGGAGCTCCATCCGCTGCCGCCAGTGTCCGGCCCTC (SEQ ID NO. 372)

Clone Rv2

:::::::Rv2SP6.seq:::::::
 CCTGCATCCGGCTCGTATGTTGTTGGAATTGTGAGCGATAACAATTTCACACAGGAAACAGCTATGACCATGATTA
 CGCCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTCACGCTCCGATCCCCCTGCCCTGATACGCGTCGGCAACCGTGAA
 CGCGATCTCGGCACCCTCGGATCGGTTCATCCGCACAAAACCGCGCTCGGCTACGGGTCGTTCCGTCGGTCAC
 CACCCAGACGAAGTGGTCGACGTAGTCAGTTCCGACAGGTAGTGCATCAACGCCGGACTGGAAACACNAGCCGACAT
 GAACCGTCGATACAGCGTCTCNCGGAGAACTGGATGTGTCGTGACGGTCCGTCGCGTCACCAGGAGACGA (SEQ ID NO. 373)

:::::::Rv2T7.seq:::::::
 CAAGATGATGCCGGTGCACCCGATCCGTGCCCTCGGTAGCGCGAACGTGCTTCCGGTCCGGCACCACCATGTC
 GCACGCACCGACCAGGCCAACCCGCCGGCGACATGCCGTTGATGGCGCCGACCACCGCAGCGGCGACTCGAC
 GATGGCGCGAACAGCGCCGTATTCCCGCGCCCGCCACCGCCATCCGGTACGGATCACCACCAACCGCCGGC
 CTCGCTGAGGTCCGCGCCGGCGAGAACGTTCCGCGGTATGCCCCAGCAGCACCAGCGCACGCCGGGATCTGCTTC
 GGCGCACTAGCCCTTGATGTAGTTGGCTGACCGAGCGTCTGACAGCGCTGGTTGTGCGGAGAGTTCAAGTGT
 CAGCCTGGCGAAGGGCCGCCAGGCCGGGAGCGTAGTCGACGGGCTG (SEQ ID NO. 374)

Clone Rv301

:::::::Rv301SP6.seq:::::::
 CTCAGCTCGATCGACAGTACTCCGCCTTGGGCTGGCTTCGAGCTGGTCGGTATGGTCGGACCTGCTGGTAGT
 GGGGATCTAACCGAACATGGTCGGGATTCTCATCGGTGATACCCATTCCGAGCTGCCGGTAAACCCCGC
 GATGCCGGGATTTCCAGCCGACTAGGATGTCTAGCCGGCAGCCGCTGCCGCCGGACTTCGGGATGTTCGGTATACC
 ACCGATCGGCAATCTGCNTATCCGCCGATGCTCGAACGCTAGCCACCCAAACCAACACTGTGACNACAATC
 (SEQ ID NO. 375)

:::::::Rv301T7.seq:::::::
 TGAATTCCCGATCCCACAATCTCGGTCAGATACAGGTGCCATACCCCTTACTTCGGCAACGCTGGCGGATTGGC
 CCTGCCGCTGCCAGCAGACCATCGACGCCATCGAATTGCCGCAATCTCGTCAGCCAATCCATACCCATCGACATTCC
 GCCGATCGACATCCGGCCTCCACTATCAACGGAATTGATGTCGGAGGTCGTCGCCGATCGATGTGTCGACAT
 TCCGG (SEQ ID NO. 376)

Clone Rv302

:::::::::::Rv302SP6.seq::::::::::

TACTCAAGCTTGAACGCTCGAGCGAGCCCAGTGTAGAGCGTTGGTACCAAACCGATCGGTGGCCAACCTGCCATGG
 GCTCACAGCGGTATCGCGAGCGTGTAGCCGATCATCGGCCAGGCAGCGACGGTGGCCTGAGCGGCAGGGTTGCCCTATC
 CATCCTCTTGGCATGGTGCAGGGAGTGCCGTAAGTCTGGTGGCAACCTGGCCCTGCGGGTTGGGTTCG
 GATTCCTCGGCTAGTAAGGTGCTCGCTGGTGTACAAACGAATCGCTAGACAGCTTATCGGGACTGCCGTCGCG
 ATCGTTGCCTGCCGATCGCTGGCNTTACCGCACCAGTCCAAAGGTGCGCTCATCGGCTCTAC
 GGCCATCTCGCCGATTCTCCNGCGTGGT (SEQ ID NO. 377)

:::::::::::Rv302T7.seq::::::::::

GCCTGTCTGAACCTCGCCGTTCCCTCCAGCGCATTGAGCTTCAGCCGACCGCAGGTAGGGAGTCGGCATGCCG
 CCTTCGCCCCGACCCCGCTGGCTAAATAGCCACCCCGAGCGCGTACCGTCTTGACCCGGACGACGGCATACCG
 GCAGCGGAACATCGCCGCGGCTGAGCGTGAACGTCGAATACGAGTCGAACAGTGTGGCGCTAAAAACCCGAGC
 CGCGGCGTCTCGGTAATCAACGGCTCCTGCGCAACCAGCTGCAANTCNGGTGCCACCGGCTTGACAAATCTGA
 TNTCGCGACCTCGCGACCCAN (SEQ ID NO. 378)

Clone Rv303

:::::::::::Rv303SP6.seq::::::::::

TACTCAGCTTGGCTCAGGTGGTGTCTGGTAAAGTTCTGAACGGTCAGGTTTCGACAATGTGGTGCCTTCG
 GCCTGTCTGAACCTCGCCGACCCCGCTATCGCAGGCTACCGTACAAACAAATCGGGTATCGTTCT
 GAGCATGAGTCGGCGACCGTCGTATGGTCGACACCCACGACGGAAAGACGCGAGTCGGCTCAAGCNGTGTGCCG
 GGATTATCAGGACTGACCTCTGGCTGACCGGCTGTTGGTCNCATGCCTGGCGCCACCGGCTTGACAAATCTGA
 (SEQ ID NO. 379)

:::::::::::Rv303T7.seq::::::::::

CATCACCTGGTTCATGAAAATGGAAGCAGCGCAGCGCTTCCCTTTCGGCGAACATGAGCCAGCCTCTCGTGGCG
 TCGGGTGCAGGTGCTGGCGAGCTGGCGACAGCCGCTGACCCCTGAAACCAGCTCCATATCCCGCAGCAACG
 ACGCCAGTCCGCTACGTAACCCCTCCGACTGTCATGGACAACANCGCTTCTCACCGACCGGGCCGGGTGTGG
 GGTGTT (SEQ ID NO. 380)

Clone Rv304

:::::::::::Rv304SP6.seq::::::::::

CTCAAGCTCCGGCCAGTACCGAAAGCGCGAACAGCTCGGGCAGCCCACACNTGCTCGTGGATTGCCG
 GCGCANATCAATTCCAGGCAGCTCCCGACAATCGGGCTCTGCTGGCCGCAACGAAGGACTCGAGGTACCCGGTG
 CCCGGGGTCTGGTGCACCTGCGATCGCACAGGTTGGCCACAACCGGCGCTTGTATGCCGCTGGCAAGCCGGC
 AGTTGCCAACCCAGCGTACAGGCTCGGCTCGCGAGTTGGCGAAGAAGTGGCTCGCTGATCACCTACCATCGC
 CAGGATCTCGTGTACACNACGCTCGCAAGGAGGGTTGTGGT (SEQ ID NO. 381)

:::::::::::Rv304T7.seq::::::::::

GCCACGTTTCCGGCCCGGCATACGGCGCGTACCGGATCTCCGCTCATACACCCCGGGTAATCGCCGACGGTGC
 CGGTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTCCAGGTCAGCGGGTGGCGCAGCAACGGCGAGCT
 CAACGACGTCAATCACGGTGTGCTTCTACGGTACCGACCCGGTACCGTAGTCGCCCCGGTGCCTGGCCGAGAA
 GTTGACCGCCACCCCGACACCGCTTGCACCGGACGCCACCCCGGATCGGGTGTGGCCAAGGTAATTGGGT
 CATTCCATTGACGGGACGCCGACCCCGAGCCCCAGTACCGCCACGACCAACGCCGGCTGACCCACCACTGTACGA
 ACACCAAGGCAGCGCCGACCA (SEQ ID NO. 382)

Clone Rv306

:::::::::::Rv306SP6.seq::::::::::

CTCAAGCTTGTGCGCTAAACCGAACGCGTACGACGCCACCCACCGCGGGTGGCCGGGGGGGGGGGGGG
 CGCCAGGCTGCTCCGCTGGTGTGGCACGCCACCGCAGACACCACCCGGCTCGCTACGTCAAGCCATACCGGGCGGA
 GCTACATCGGCTCGGCCGCCAGTGTCTGGGCCCTTTCGAGGTCNAGGTCNATACCGATTGCGCATCCGAGCCG
 CACCCCTGGACGACAGAACCGTGCCTACGAGTGTGCTGGCGGGGCCAAAGAACANCTTGGCATCCTGGCGGATT
 GGCGCGCGGGTCTGGT (SEQ ID NO. 383)

:::::::::::Rv306T7.seq::::::::::

CTCGGGTACGCTTCGGTGCAGTGTGCGAGTGATAGATGACGACCGGACCTCGTGGCATCTTCCATAGCCGCCAC
 ACCTTCAGTTGCTCACCGGAATCCAACCGGTANAANGTGGCGAGCGCTGGCATGGGATATGCCGCTCG
 GGACGGTACAGGCCCTGGTCCGGCAGCACTCCGAGGCTCGTGGGTGGTGCAGNCGCATGGCCACCATC
 GCATTACACCAGGTCTGCGCG (SEQ ID NO. 384)

Clone Rv307

:::::::Rv307SP6.seq:::::::
 CTCAAGCTTCAATTCCCTCACGACGCGTTCCCAAATGAATTCCGATCCCACAATCTGGTTAGATAACAGGTCGCC
 ATACCCCTTACTTCGGCAACGCTGGCGGATTGGCCCTGCCGCTGCAGCAAACCATCGACGCCATCGAATTGCCGGCA
 ATCTCGTTCAGCCAATCCATACCCATCGACATTCCGCCGATCGACATCCGGCCTCACTATCAACGGAATTTCGATG
 TCGGAGGTCGCGATCGATNTNTCGTCNACATTCCGGNGGTCAACCACCGGGACCAGNATCGACCCGATTCCG
 CTGAACCTCGACGTTCTCAGCAGGCCGGAACCA (SEQ ID NO. 385)

:::::::Rv307T7.seq:::::::
 TTAACCCCCGTCGGCTCTACGCCCTNCGGGTCGAACATGCATCCGAGCANATGCTCGAGCGGCACCCACTCGC
 CGATGGCCGGAACCGGCTGGTACCCGGTGGCGGCTGACGTTCCGGCAGGACATCGGCTGGGAAGGGCGCTTG
 CCACCGTCGTCGAAGACCCAGATTGAAAGGTGTTCTGCTGCTACGACATGACCCGGGACGAGAAGAACCTTG
 ACCGGTGGAAAGGCTCCGAGTCGGCATCCACCANAAGATCCGATGCCGTT (SEQ ID NO. 386)

Clone Rv308

:::::::Rv308SP6.seq:::::::
 CTCAAGCTTGTGATTTGATCATCATGGATGATCATCACCGAAGTGTGGTAGCCGAGTGGTATCGTGGTACCGTGC
 TGCTTCCATGGCGCCTTTGGGCTTCCGTTGGCTGGGACATTCTGGGTATCGAGTTGACTGGATGG
 TGTTGGCGATGTCGGTATCCTGCTCTGGCGTGGGATCCGACTACAAATCTGCTGCTGATTTCCGGTTGAAAANG
 AAATTGGGCGGATTGAAACACCGGATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTACGGCTGCCGGCATGG
 TGTCGCCGTTACCATGTCGTTGGTGTGCAAGCAGATTGGTCAAGT (SEQ ID NO. 387)

:::::::Rv308T7.seq:::::::
 CGNCCAACCCGAATTGGTTTCGGGCCNTCGGTGAGGACGGCGTGCAGGTCGCTCAACGACGACGTCGTCGCCGGAC
 ACACCTCGATGCTGCCGCATGGACGCCGTCGAACGCAAGCAGCTGATCGAGCTAACACGCCGCCGGAACGCTTCCG
 CCNCNGCGTTACCGCATCCGTTGACCGGGCGATCGCGGTGATCGTCGATGACGGCATGCCACCGGAGCGACGGC
 CAAGGCGCGTGCACGGTCGCCCCGGCGACGGTGCAGGACAAAGTGGTCTGGCGGTCCCAGTCGGCCANACGACAT
 CGTGGCGAGATTGCCGG (SEQ ID NO. 388)

Clone Rv309

:::::::Rv309SP6.seq:::::::
 CGTGACTGCCACCGGGGCCACTCCGAGAACATCTGACCCGACCAAGATCTACACCATCGAATACGACGGCTGCCGA
 CTTTCGCGGTACCGCTCAACTTGTGTCNACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACACTACTT
 CATCCTGACGCCGGAACAAATTGACNCAGCGGTTCCNCTGACCAATACGGTCGGTCCACGATGACCCANTACTACNT
 CATTGCAACGGANAACCTGCCGCTGCTAGAGCCACTGCGATGGTGCCTGACGGGAACTGGTGGTGGGAAACCGACATGGT
 TCAACCAAACCTGAAGGTGATTGTTAACCTGGGG (SEQ ID NO. 389)

:::::::Rv309T7.seq:::::::
 TCGCTCAAGCGNTGAGGCCGAANCGCTGGTACGACTCCCTGTTGTGATGGACCAACTTCTACCAACTGCCCATGT
 TGGGACGCCGACCAGCCGATGCTGGAGGCCTACACGCCCTGGTGCCTGCCACGGCAGCGGGCTGCAAC
 TGGCGCGTGGTGACCGCAATACCTACCGCAGCCGACCCGCTGGCAAAGATCATCACCACGCTGACGTGGTTA
 GCGCGGTCGAGCGATCTCGGCATTGGAGCCGTTGGTTGAGCTGGAACACCGCCAGCTGCTTCGAGTTCGGCA
 CTTTCAGTGACCGGTTCAACCGCTCGAAAAGGCCTACANAT (SEQ ID NO. 390)

Clone Rv30

:::::::Rv30SP6.seq:::::::
 ATACTCAAGCTCCGCTGGGCCTGTTCAACCATGGCAGATCCGTTGGTCCCAGATCCCGAACGAGGACACCGCGA
 CCCNCTCGGTGATGATCATTACCGTTGGGCACTGCGTAACCGCTTGCAGCACAAAGAGCCGGTCTGACGCTCG
 AAAGCTCATCGGGCACCGATTGAAATGCAAGCAGCGCCGACCCACCCGCTGCCGAGTGACAGAATTGCCCTGATCA
 GCCCGACGGTCCCCGCCGATGCCGCTGTGCCCATGTTGCTCTTGGCGATCCAAGCGCGCAGGGGGTGCCCGCGC
 CATAACCCGCCAGGCTGCCGACTCAATGGTCGCCGATTGGCGTACCGGTGCCGTGCCCTCCACCAACCGA
 CCGTTCGGGCTG (SEQ ID NO. 391)

:::::::Rv30T7PEG.seq:::::::
 CAACAGCGTCCAGCGGCATACCAACCGCACATGCCGTGCAACCGGCCGGAGTCGCCGATAACACANGTACA
 CCTTGGGAATCGGTGTCGCCAGGGATTTCNACCCGGGGTGGGCCGATGCCGCCAGGTCGAGTTGGCGCGA
 CGTGTGATNTCACCGCCGACGTAGTTGGCGTTGTCGCCATCCGCGCCGGACGGCGGGCCACCGCAGGCGC
 TGTACCGGAAGCCGGGGCGAACGCTCGACGACCTGGTACCGTCTCGCNCNTCAGTGGACCCGACNGCACGT

GGGCATATGTCCANAACGGACGNGCCGGTTCTCGATGCNGCCGGGTCCGCGACNTGCGAACNCNCNGNCACACC
ATCCGCCAGTCGCGTGGCGTCCC CGCGACTCTGCCCTGGCCGCGCA (SEQ ID NO. 392)

Clone Rv310

:::::::Rv310SP6.seq:::::::
CTCAAGCTTGNCGACGATCGGGCGATGTCGATGANAGGAAACCCAGCGCACAAACGACNATTGGCGTAGCCGGC
GGACNTCTGCTCGATTCCGATCACGTCGGCGCTCGCATCGAGCATGGCGCCGGCAGGGTAGCAGCGATCCGCCGTC
GTCGAGGAACACGACACGAGCCGTACGCCCGCGTAAGCCGCCCCAGGATTGGCGAAAAACGTTCTACGTGGCG
GGTGTACTGGGTGTCATGATTGTCGGGTGCGTAGGCCTGCTGCAATGTCGACATAATGCCGTGGCCGAT
CGCGTCAACAACCTCCGGGTGAGTGGAAATANCACTTGCCGA (SEQ ID NO. 393)

:::::::Rv310T7.seq:::::::
TCCAACGCGGTGACAGATTGTCTATCCTGGACCTGACGGTGAGGTGAGGTCGAAGTTCCAGGAATTGGCAAAATCGGTA
AGAGCCTGAAGAATTGCGTATGCCGACGAAATCTGCAGGCATACGGGGCAGATACGCTTCGGGTTACGAGATGT
CGATGGGGCCGCTGGAGGCTTCACGTCATGGGCACAAAGGATGTTGTCGGCGCTACCGTTCTGCAAGCGGGTGT
GGCCTTGGTCGACGAGCACACCGCGAAACTGGGTGGCTGACGGCGTGGAACTCGACATCGATAACGCTACGGG
CGTGCACCGCACATCGTGGCGTGT (SEQ ID NO. 394)

Clone Rv311

:::::::Rv311SP6.seq:::::::
CTCGTCTTGACTACGCCAGTATGAAACCTCCTGTGCCGGTNCGCTAAACACCAGGCGGACACTCANACGGTGCT
GGTGTGCGGCATGGCACCGCGGGCAGCAAAGCGCACTTCTCCGGGACGACAGCAAGCGACCGCTAGACAAGAGGG
TCGTCGCAGGCAGAACGGTTGGTACACAGCTGCTGGCGTCCGGCCACCGATGTTATGCCGCCACGGGTGCG
CTGCCACCANACNATGGAGCCACTGCCGCGGAACACTGAAACGTGACCATACACAACGAGGCCNCCTGACCGAAGAGTC
CTACGCCAACACCCAAACGCCGACACCGAGTGCTGAGATCTCG (SEQ ID NO. 395)

:::::::Rv311T7.seq:::::::
GTATGCCCTCCNCCCTTGGCCACCAGCAGGCCACAGCGGGTTCGCGGACCGAACGTGGACATCAATAGCCCGAATCG
GTGTGTGCAAGTTGGTAAACGGTGTGATCCCAAGCTTGCAGCCTTTCTGAGTCTTGGGCCCCACACCCACAGT
GCTTCGACGGTACGGTACCCATGATGCCATCCAGTGGCATCGGTGAGCTGATAGATGCCAGCTGGTTTCGCCAAC
CCGGTAGCGATCTGGCGCTGCTTGTGACTGATACCTATCGAGCAAGACAGCCGGTTTGCAGACAAGATGACT
TTTGGATCTCTCNGCAACTCCAATGGGGTCTCCGGGANT (SEQ ID NO. 396)

Clone Rv312

:::::::Rv312SP6.seq:::::::
CTCAAGCTTTGGTCTAGCCGCCGAGCACGATACGGGTGTCCTGGCACCCGGCGGGCTGTCGGGAAATGGCGG
GTCCCCGGTGGTTTGTGANGANTGCTGAACCGTAGTCGAAGTGGCGCGTCAGACTCCACCCAGCCAGGCAG
CGCGAAGCTGAATCCTCCAACCGGGTTGTCGATCCGACAGGTTGGGTGCGTTGGGCAATGACAGGTGGCGGGCG
TGCCTTCGGGTCGGCCGGCGAGGTGCTGCGTTGGGATCNCCCGCTGGCATTGCCNTTGGCGGGCGGGTGG
TGGGGGGCACANGTGTCCGGTGGGGTGGCGCTGC (SEQ ID NO. 397)

:::::::Rv312T7.seq:::::::
ATCTGTACCCGACCAAGATCTACACCACATCGAATACGACGGCGTCCGACTTCCCGGGTACCCGCTCAACTTGTG
CGACCCCTCAACGCCATTGCCGACCTACTACGTCGACTCCAACTACTCATCCTGACGCCGAACAAATTGACCGAG
CGGTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTACATCATTGCAACGGAGAACCTGCCGTGCTAG
AGCCACTGCGATCGGTGCCGATCGTGGGAACCCACTGGCAACCTGGTCAACCAAATTGAAGGTGATTGTTAAC
TGGGCTACGGCGACCCGGCTATGGTATTGACCTGCCGCC (SEQ ID NO. 398)

Clone Rv313

:::::::Rv313SP6.seq:::::::
CTCAAGCTTGCAATGCCGGTGGGATGCCATGGTGGAAANATGGTGCCTGGCGTCNAATACGCGGAGCGCATGA
GCTCACCGGTTCGGAACACGTATCGAAAAACGTCGCACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTGTA
TCCCAACTCTAATGCTGCTATCGGATCGCGTAATCGANATATTGCAATGCGATGACAGGCCGCAATCGGTT
ATTGCTTACGCTTCCCGGGTCGATCGTGTGATGCACTGCCGAAAACGCCGATATGATTGTAACCGTATCTA
ACGCAATTATTGATGTGGTAGGGCGCAGCTGCCGTTTGTGCTGCG (SEQ ID NO. 399)

:::::::::::Rv313T7.seq:::::::::::

400
 CAAATACACGCCGGACCGCACAGGCCACATGCCATCCCGAGCACACCCAAAACGGGATACAGGATGGAGGCCAACGC
 CACGGCCGCCAGGATCACCAACACACCGGCTTGGTCAGCTGTCGGCGCGTATAGGCATCGGCCGCTGCAA
 CGCAGCATGCACAAACCGCTACACCCTGTACCCAAGACGCCGACCAGCAATACCAAGCATGACGGTACCCACGAGGTG
 GCTCACGCATTAGACTATGCGGTTGCATCCAACACG (SEQ ID NO. 400)

Clone Rv314

:::::::::::Rv314SP6.seq:::::::::::

CTCGTCCTTCGGCCTCGCTGCAGGAGTGGAGCCGAGGGCTGGAAATCCGAAAACGAGCCGGTGTGCACTGTGCG
 CGGATCGGCCGCGCACCTGGTGGTGTACGGATGAATCCGAGCGAAATGTGGCTGCGGTGGCTGACTCGT
 TGGCGTGCACGCTGGTGGCAGCCACCGAGCGGTTGGTCCAGGATCTGGATGGCAAGTTGTGCGGGCCCGCCGGTGA
 CGGCCGATGAGCTGACCGAGGTGACAGCGCCGTGTTGGCTGACTTGGAAACCGACATGGAGTCGCCCGGTT
 (SEQ ID NO. 401)

:::::::::::Rv314T7.seq:::::::::::

GTCTAGNCCCGAACACCGATACGGGTGTCATTGGCACCAGGCGGGCTGTCCGGGAAATGGCGGTCCCGGGTGGT
 TTGCTGAAGANTGCTGAACCGTAGTCGAAGTGGCGCGCTCAGACTCACCAGCCAGCGAGCGGAAGCTGAA
 TCCTCCAACCGGGTGTGATCCGGACAGGTTGGGTGCGTTGGGCAATGACAGGTGGCGGGTGCCTGGGTC
 GGCGCGGAAGTGCTGCGTTGGATCGCCCGGCTGGCATTGGCGTGTGGCGGGCGGTGG
 (SEQ ID NO. 402)

Clone Rv315

:::::::::::Rv315SP6.seq:::::::::::

ACTCAAGCTTGAGATTGGCGTCAACGGGTGTCGGCACGGCGTCTGCAGTTGGTAGGCCTGCAGTTGTGCATCAGG
 CCGATGCCGCGCCCTCGTGGCACGCACTGACANACCAACGCCGCGCCCTCACGGCGACCATCGCCAGCGCG
 TCCAGCTGAGGCCGCAATCGCAGCGCGTGAACCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGACAGC
 ACGTCG
 TCACCGTCGGCGTTGGGCCGGGATCTGCCGCGGACAGCGCAGATGTTCCACGTCTCGTAAATGCTGGTGAN
 CGATGGCGCAAACCTCCCATGACAANTCGGAATCCGCGCTGGCACCCGCTCAATGTTGCTCTCTGCTTG
 (SEQ ID NO. 403)

:::::::::::Rv315T7.seq:::::::::::

TCGACAGCATTCTGACNGTTGGCTGGCATGGTAGCCAAGGTTCTGCGGTCCCACAGATCATCTGGTC
 CGGTAGCGCTCGTCCGGGTATGCTGCCCGGGATTCTCGCTGCTATTACTCCCCCGAAGAACGCCACGGTCCAGC
 GCGTGGGCCGCGCGGTCCCCATCACAAACTGAACCCCAACAGGGACATGCTTAGCGTAGGGCGCGCCAAGGC
 GGCAGCAATCGCATCACTGCGCTGCCGTCACTATTAAACCCACCCGGACTTCACTTCCACGACCCGAATGGCGCCCG
 GTCAATTGATCATCTGGCACCAGCGGATAATCCGGGAT

TG (SEQ ID NO. 404)

Clone Rv316

:::::::::::Rv316SP6.seq:::::::::::

ACCGGGGCCACTCCGACAATCTGTACCCGACCAANATCTACACCCTGAATACGACGGCGTGCCTGACTTCCGCGG
 TACCGCTCAACTTGTGTCNACCTCAACGCCATTGCCGCCACCTACTACGTGCACTCCAACACTTCATCTGACG
 CGGAACAAATTGACGCNGCGGTTCCGCTGACCAATACGGTGGTCCCACNATGACCCACTACATCATTGCAAGC
 GAAACACTGCCGCTGCTAAAGCCACTGCGATCGTGGCGATCGTGGGAAACCCACTGGCGAACCTGGTTCAACCAAAC
 TTGAAGGTNATTGTTNACCTGGGCTACGGCGANCCGGCTNTGGTTATTCCACCTCNCCGCCAATGTTGCNACTCC
 CGTCGGGGTTGTTCCCNNAAGGTCAACCC (SEQ ID NO. 405)

:::::::::::Rv316T7.seq:::::::::::

CGCTCAAGCGCNGAGGCCGAACGGCTGGTTACGACTCCCTGTTGTGATGGACCACTTCTACCAACTGCCCATGTT
 GGGGACGCCGACCGAGCCGATGCTGGAGGGCTACACGGCCCTTGGTGGCGTGGCACGGGACCGAGCGCTGCAACT
 GGGCGCTGGTGGCAGCCGAATACCTACCGCAGCCGACCCCTGCTGGCAAAGATCATACCCACGCTGACGTGGTTAG
 CGCCGGTGCAGCGATCCTCGGCATTGGAGCCGGTTGGTTGAGCTGGAAACACCGCCAGCTCGGCTCGAGTTCCGGC
 TTTCACTGACCGGTT (SEQ ID NO. 406)

Clone Rv317

:::::::::::Rv317SP6.seq:::::::::::

CTCAAGCTTGGCTTCGATGAAGTAGTCGTCGGTCAGCGCCGCCTTCTGAGCTCCTGGCGATGCCAGCAAGGAGTC
 ATCGCCGCCGAGCTTGGCAGGATCTTGTGCGCTGTTCTTGACGATGCGGGCCCGGGATCGTAGTTCTGTAGAC
 ACGATGACCGAAACCCATCAATTGACCCGGCCTCGCGGTTCTGACCTTGCCTACAAACTCGCTGACGTGCGCC

GCTGTCGCGAATGCCCTGAGCATTCCAGGACAGCCTGATTGGCGCCGATGAAGCGGACCCATAGTGCCTTGAT
GCC (SEQ ID NO. 407)

:::::::Rv317T7.seq:::::::
GGTCAGGCCGAGCAGGCCGAGGAACGACGAAACCAACAAGCCATGGTGGTGGCGCCGTCGAGAGGTGGCGGTGCGC
CACAAACGGAAAGATCGCCTTGAGCGTCGCTGACCGCCGCTCGAGTTGGGTCTAAACGAAGTAGCTGATGCCGATCA
TGTGACGTTCCGTCGATCAGCGTCAGCGGACCCACTCNACGAGGTCTCGGTGCCGCCAGGGCACCA
GCAGTGACGAGTCCAGGCCGCTGGCCAAGCAGTCGGTGCCANCCGTGGTGGGTGGCGATGGTGGGTGTG
TCATTTGGAAACGCCA (SEQ ID NO. 408)

Clone Rv318

:::::::Rv318SP6.seq:::::::
CTCGAAGCTTAAACAGCATCAACCCCGCCCCGACCGACACNATGTCATGCCATCGAGGTGAATGTCGAA
TGGCGCAAACCATCGCGACCGCAGCCACATGGTACCGCGATTCCGGTCCAATGCCACCCGACGG
CCGCTCTCACCGCAGGTGACCTCGATACCGAGACCANCCGGCGTTNTNTCACGACCCCTACCGTGTACGCCA
AAACGGCGCTGGTGGTCATTGCCGGAGTGCACCCNCACCCAGTGTGCCCCGATCC (SEQ ID NO. 409)

:::::::Rv318T7.seq:::::::
TGATGCCGACCCGATCGACGGTCGTTGGTCGGGGTTGACTGGCGCCCGCGAAGCAGGGCGTCGACCGCGGCGCG
ACGTCGGCGGCCGTACCGGTGGCCATTGCCCGGGAGTCGAGCTGACCGAGCTGACGGTAGACAAGTCGGCGCTGG
CCGTCGAAGACNAACGTGTCGGGTGTCAGGCCGCGAGAAGGCGGGGACNTCTGGGTTTCGTCGTANAGATAC
GGGAACGTCCAGCCGTGGCGGGCCTGGCGACCATCTGATGGGCCGTCC (SEQ ID NO. 410)

Clone Rv319

:::::::Rv319SP6.seq:::::::
TTTCGGCGAGCGGTATANCTCCCTCGTACCGCGACGCCAGCCGANAAGCTCGTTTCCAGTGTGCTGGGG
ATTCTCACGCTGCTGCTGANTGCGTGCCAACCGCTCCGCTCGGGTACAACGAGCCGCGGGCTACNATCGTGC
ACGCTGAAGTTGGTGTCTCCATGGACTTGGGGATGTGCGTGAACCGTTCACCTACNACTCCAAGCTGGCGCCGTCT
CGTCCGAGGTGCGTGTGCGATAGCGGGAGGCCGGAATCGCAATGACGGATTCCNTGCCANCCTCCGAGTTGC
NTGCGGATGACTACNAATTGATCACCCANAACCATCGGGCGTTACTGCCTGAAGTACCTGGTGCAGGGTGGATAC
TGCTATCCGGCGGTGACAACCCCGCAAGC (SEQ ID NO. 411)

:::::::Rv319T7.seq:::::::
GTTTTGGCTGGCATGGTAGCCAAGGTTCTGCGGTCCCCACAGATCATTTGGTCCGGTAGCGCTCGTCCGGGTATG
CTGCCGCCGGGATTCTCGCTGCTATTACTCCCCCGAAGAACGCCACCGGTCCAGCGCGTGGCGCCGCGGGTCCCA
TCACAAACTGAACCCCAACAGGGACATGCTTAGCGGTAGGGCGCGCCAAGCGGCAGCAATCGCATCACTGCGCT
GCCGCTCACTATTAACCCACCCGGACTCACTTCCACGACCCGAATGGCGCCCGGTATTGATCATTTGGCGCACCG
CGGATAATCCGGGATTGCCAGCCATTNACTACCGCATGCGAGTCATCGGCTGACCGCAGCGGT
(SEQ ID NO. 412)

Clone Rv31

:::::::Rv31SP6.seq:::::::
TCGCCTAGGCCGGCTTCCCTTCCGTCGAGCNGTCAGAACGCTCTATGACAATGCACTACCCGAGACNATCAACGGC
CTATGCAATACCNAGCTGATCAAACCCCGCAAGCCCTGGCGTCCATCGAGGATGTCGAGTTGGCCACCGCGCCTGG
GTCGACTGGTCAACCATCGCCGCTCTACCGGTACTCGGGGACATCCCGGGTCTAACTCGACGCCGCTCACTA
CGCTCAACGCCAGAGACCANCCGCCGCTGACGTCTCAGATCAGAGAGTCTCCGACTCACCGGGCGTTCATCCCC
ACTGTCGATAGCGTGTGGATAACTTGTCTGCA (SEQ ID NO. 413)

:::::::Rv31T7.seq:::::::
GCGCGTNGAACTGATAGGTGCGGCCGGCTCGAGCANGCCGCCATTGTTGATGCGGTTACCGAAGATCTTCGG
TGACCTGCCGCCGCCGGCAGCTGCCCGAGTGCCGGCTGGCCGCCGACAATCTGGCTCCACGGTGG
TCTGGGTCA (SEQ ID NO. 414)

Clone Rv321

:::::::Rv321SP6.seq:::::::
CTCAAGCTCAATACAGAGTTATAAACTGTGATAATCAACCCCTCATCAATGATGACNAACTAACCCCGATATCAGGT
CACATGACGAAGGGAAAGAGAAGGAAATCAACTGTGACAAACTGCCCTAAATTGGCTTCTTAAATTACAGTTC
AAAAAGTATGAGAAAATCCATGCAGGCTGAAGGAAACAGCAATAACTGTGACAAATTACCCCTAGTAGGTAGAACA

ATGTGACGAACCACCCCTCAAATCTGTGACAGATAACCCTCAGACTATCCTGTCGTATGGAAGTGATATCGCGGAAGG
 AAAAT (SEQ ID NO. 415)

Clone Rv322

:::::::Rv322SP6.seq:::::::

CTCAAGCTTCGATCGACATTACTCCGCCCTGGGTCTGGTCTCCGAGCTGGTCGGTATGGTCGGACCTGCTGGTAGT
 GGGGATCTAACCGAACATGGTCGGGATTCTCATCATGGTGTACCGTGTACCCATTCCGAGCTGCCGGTGAACACCCCGC
 GATGCCGGGATTCCAGCCGACTAGGATGTCTAGCCGCCAGCCGCTGCCGCCGACTTCGGGATGTTCGGTATACC
 ANCGATCGGAATCTTGCATTCGCCGATGCTCGAACGCTANCCACGCCAACCAACACTGTGACNACAATCGCCA
 CCACACCAAGGTATGCCCTCGCGTGTATGCCGGTGCAGAGCTCCGACGCCGCC (SEQ ID NO. 416)

:::::::Rv322T7.seq:::::::

CATTCCCAATTGAATTCCCNATCCACAATCTCGGTTCAGATAACAGGTGCCATACCCCTTACTTCGGCAACGCTGG
 GCGGATTGGCCCTGCCGCTGCAGCANACCATCGACGCCATCGAATTGCCGCAATCTCGTTAGCCAATCCATACCCA
 TCGACATTCCGCCGATCGACATCCCGCCCTCCACTATCAACGGAATTTCGATGTCGGAGGTGCGCAGTCATGTGT
 CCGTCGACATTCCGGCGGTACCCATCACCGCACCGAGATCGACCCGATTCGCTGAACCTCGACGTTCTCAGCAGCG
 CGGACCCATCAACATCTCGATCATCGACATTCCGGCGCTGCCGGCTTGGCAACTCGACCGAGCTGCCGTCGTCGG
 GCTTCTCAACACCGGGCGGTGGCGGCT (SEQ ID NO. 417)

Clone Rv327

:::::::Rv327SP6.seq:::::::

CTCAAGCTTCGGCGAGACGGACANNTTGCAGAACATTGATGACAAAATAGAAATCATTGATGGTTGAGTCACCAGG
 CCGATCAAGCCTCGCCGAGCCAATTCCAATCAAGAGGCCAACGCCCCTACCAATCAGCCCGCAACGAGGGATTCC
 GTCATTATCAGCCAAAATAACTGCTCTCGGTTACACCCAAACAGCGCAATATGGGAAAAACGGTCGCCGTTGCACG
 ACATTAAATGTCACGGTATTG (SEQ ID NO. 418)

:::::::Rv327T7.seq:::::::

AGCTTAACGTCCCTAATACCTGGGCTGTGCCTCGGTGTATGCACGGCATACGGACATCCNTCCCTGAGACCCN
 CGGTCTAACTAGCCACGTGTCCACCATCAGGGTCAACCCCGCCAAGGGCGACGCCACCCCAAGTTGCCGACCGTT
 AACCTATTGCTGTGAGCTTCATTGCTCGAGCAAACAGTTGGTCGGCGTTAGGAACGATGACACTCAACCGA
 TTTGGTGCNCCTAGGTGTCCCTGGCTCGGGTGCCTGGTGTGTCCTGGCTGTGGTAACGACCCAAATGTGACCGGG
 GGAGGTGCAACCACTGGCACCGTCCGCAATGCTATTGCCGGGG (SEQ ID NO. 419)

Clone Rv328

:::::::Rv328SP6.seq:::::::

CTCAAGCTGGGTGGCGCTGTCGGTGTGCTTGGCGCGTCGGTATCAACACGCCACGAAATGGGCACAAG
 AAGGATTGCGCTGGAGCGGGTGGCTGTCAAAATCACCCCTGCCAGACCTGCTACGGCACTTCTACATCGAGCACAAC
 CGTGCCATCACGTCCGGGTGTCACACCGGAGGACCCGGCTGGCGCGTTCGGCAGAACGTTGTGGAGTTCTCTG
 CCGCAGTGTATCGCGGCTTGCCTGGCGTTCAATTGGAGGCCAACGGCTGCCTGGCGTCAGCCCC
 CT (SEQ ID NO. 420)

:::::::Rv328T7.seq:::::::

GCACCAAGGCCAACACGTCAACCTGTGACCTCTGCCGACCCGCCAGGGTCTGGCCGTTACCACTGAAACGG
 GCGAGCCGGAGTCTGGTACGCAACAAAGAGCAAGGTGCAATGGCGGAGTTGTCGACCTCGTCACTGAGACG
 GGGTCNATCCATTGAGGTCGCGCTCGCCGCTCGGTGAGTGGCGGTACACTCCAGGTACTCGACCTCACAGACGAGA
 GGACTCGATCCCATCTAGGTGTGGACAAACAGATCTTCTGTCGA (SEQ ID NO. 421)

Clone Rv329

:::::::Rv329SP6.seq:::::::

TCGCCTCCGCATATGGGTGACGCCAGCGGGTCCGGATTTCTGGGCTTCATCGCTCGGCCGCGACAAACAGCG
 CGGTGCAACCGACACTCGTGTGATGTCAGCTATCACCTCGGTACGCCAACCTACNCGGCTATCTCA
 GCCCGATCTCAGGCTCCGCCAGCCAGGTGCATCCGGATCCACTAACCCGGACCCATTGGCGTC (SEQ ID NO. 422)

:::::::Rv329T7.seq:::::::

GTCCTCGAGTGGCGCCGTCGNACNCCAGCGCCGCCAGGGCCACTTGGATGCGACCCGTTCAAGTCCCTCATCAT
 CTGCGAAAAGCCTTGACCCATGGCTCGCCAGGATCGCCGAGACGGCACCCGGAGGTTGTCGAACGACAGCTCGCA
 GGATTCGACGCCCTTGTAAACCAACTCGGCAAGTCCCGCACACCGTGAATGTCGACGCCGGGTTCGACGAGCACGAT
 CGACATGCCATTGGTGCCTGGCGGTGTGGCGTTCGGGT (SEQ ID NO. 423)

Clone Rv32

:::::::Rv32SP6.seq:::::::
 GGATACCAATGTGGACTTCTGCTCACCCACGATATCGTGGCTGATCCGCTGCTGCGGCGGGCTGCNACCTGCNTCTCNGGGCACCGTNACTACATGGCNCGCGCAGCATACTGTCGCGGGACCCACTCCNACTGGTCGACGGTGTGGCCGCGTGTCCGCGTCCNAACCCGGCGCACCGACGAAACCGGCCGCGTCCGTTCTGGACCAACGCTCATGTCGCTGGGTCCATGCTGACGCCATCGAGACCGTAACCAGCGCTCGAGCGGTTCGCCTCCGGTTCCGTGACATCTCGTGGCTGCTCGCGCGTCCGCGCGATGGTCGACCAACGCCAACCTCGCGGCGTACATCACCCTCGGCCACTCGACCTGGCGCGATCGCGGCC (SEQ ID NO. 424)

:::::::Rv32T7.seq:::::::
 GTGAGCAGACCTACGCCNCTGGTTGCGCCAACCTGGTACCGATCATGGCGCGNGCTGTCGTCACCGATACCCAGCGAACAAAGACAGCCGGTCCGCGACAAGATGACTTCTCCGATCTCTCGGCGACTTCCATGGGGTCGTCGGAGTCCCGGGCCACCGCAGGTAACCCCTCGTCTCAGTCCCATACGCGACCGGGTATCCACGTCGCGAACACGCCACCCCTCAGCAGCCNCGCTGTGACCGCGTGGGTTCCACNGCAATAAGTGGCCTCANGCATCGTCCGGCGGTCCNCAACGCA (SEQ ID NO. 425)

Clone Rv330

:::::::Rv330SP6.seq:::::::
 CTCAGCTTGAGGTTAACCTTGAACGGATCGAGCTGGACGTTGAGACGGTATCGGGCGAACCTGAATTGTCGGGAAATGCCAACCGCAACGCGAAACCGGGTGGCCGGTGAACCGGGCTCGGCGCACCGTCGAAATCTATGTCGGGATGGCCGAATGGGGATGTCGGCACGGCGAACCGTAGTTGCTGTCGGTGGAGGCCCAGGTGGATGGGGGGAAAGATCCTGGTGTCCGGATAATAATGGGGCGATGCCGGTTGAAGTCCACTGGATCGGAATTCCGAATTCTGATCCGACGTTCAGGCCAACAGGCCCTC (SEQ ID NO. 426)

:::::::Rv330T7.seq:::::::
 CGCGACGTCGCGATACGCCAGCAGTTGGGAATCGCTCTGCAACCAATATTCTGCGGACGTTGAGAGGACTTTTGAAATGGACGGATCTACCTGCGCGCAGGAGCTGGACCGATTAGGCGTACGCCCTCCGCTGGACGACACCGGGGCACTCGATGACCCGACGGACGGCTCGCGCNCTGCTGCGGTTAGTGCACGGCCAGACTGGTNTTCGCTGGGACTGCGGCTGATTCCACACCTGACCGCCGACGGCTGCTGCTGTGCGGCCATGTCGGCATCTACGCCGTCACTCGCCTTGATCAGAGCATGCCGGCGTCTGA (SEQ ID NO. 427)

Clone Rv331

:::::::Rv331SP6.seq:::::::
 CTATAAAATACTCAAGCTTGATGCCGCCAACCGAGCGTGGACGACGCCAACGCCACGCCGGGTCGGCGCCGGCCGGGAGCTCCGCTCGGTGATGGCACGCCACCGGACACCACCCGGNTGCCTACGTCNAGCCATAAGGGCGGAGCTACATCGCTCGGCCGCCAGTGTTCGGGCCCTTTGAGGTCNAGGTCNATACGATTGCGCATCCGAGCCGACCCCTGAACNACANAACCGTGCCCTACTATTGCTTGCTCNGCGGGGCCAAAAACAGCTTGCATCCTGGCCNATTGGCGGCCGG (SEQ ID NO. 428)

:::::::Rv331T7.seq:::::::
 CTTCGGTCGAGTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTTAGAAGGTCGGCGAGCGCTGGCATTGGCATCGGATATGCCCTCGGGACGGTCAGAGCCTCGGGTCCGGCCAGCAGCTCCGAGGCTTGTGCGGCGACGCGCATGGGCCACCATCGCATTCAAGGTCTGCGCGAATCNCCANCACGTANACNGTTCTTCTAA (SEQ ID NO. 429)

Clone Rv333

:::::::Rv333SP6.seq:::::::
 CTGGCACCAAGGCCCCACACGTACCCCTGTGACCTCTGCCGACCCCGCCGAGGTCTGGCCATTACCGAACGGCGAGCTGGTNCGCATCGAACAAANAGCAAGGTGCATGGCGGAGTTGTTCCGCCACTTCGTCGATGAGGGTCNATCCATTGAGGTCCGTCGCCGTCGGTCAAGTGGCGGTACACTCCAGGTACTCGACCTCACAGACNAAGGACTCNATCCCCTACTAGGTGTGGACNAACAGATCTTCTGTCGACNACTACACCCACCCAGGCCATGCCGCTGCCGCGATGCCAACCTGCAACTTCGACGCCGACTGGCCGCTGGGGGGCGCTCCCCGGTTGTCAACACTTGCCGTGTTCNTCAACGCNCTGCCACATCCAACCCCAACG (SEQ ID NO. 430)

Clone Rv334

:::::::Rv334T7.seq:::::::
 GTTCTTGGGCCATGCGGAGGTATGCCGTTCCACCGCGTGGGGTGGCGTTGCATTAGCTCACCGATGGTGCCTTGTCAGGGCGCCGGGAGTGCCTGGTAAACCATCTTGTGCTGC (SEQ ID NO. 431)

Clone Rv335

:::::::Rv335SP6.seq:::::::
 CAATACTCAAGCTTGGCGTCCGTTCAACCCGAATTGGCTTCGGCGCCATCGGTAGGGACGGCGTGCAGGGTGCATCA
 ACNACNACGTCTCCGGGACACACCTCGATGCTGCCATGGACGGTCAACGCAAGCAGCTGATCGAGCTAC
 AACGCCGCGCGAACGCTTCCGCCGGCGTACCGCATCCCCTGACCGGGCGGATC (SEQ ID NO. 432)

:::::::Rv335T7.seq:::::::
 CNTCATGATGATCATACCCGAAGTGTGGTAGCCGAGTGGTTATCGTGGTACCGTCGTGCTTCCATGGGCCCTC
 TTTGGGTTCCGTATTGGTCTGGCAGGACATTCTGGTATCGAGTTGACTGGATGGTGTGGCAGTGTGGTGT
 CCTGCTCTGGGGTGGGATCCGACTACAATCTGCTGCTGATTTCCGGTGAAGAGGAAATTGGGCCGATTGAA
 CACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTACGGCTGCCGATGGTGTGCCGTTACCATGTC
 GTTGTGTTGTCAGCGATTGCGAATTATTGGTCAGATCGGTACAC (SEQ ID NO. 433)

Clone Rv336

:::::::Rv336SP6.seq:::::::
 ATACTCAAGTTTACGGTATCGCNATCACCTGGTCATGAACGGAAAGCAGCGCAGCGCTTCCCTTCCGGCCGA
 ACATGAGCCAGCCTCTCGTCGGCGTGGGTGCAAGGTGCTCGGGCAGTCGGCCNACAGCCGCTGACCCCTGAAAC
 CAGCTTCCATATCCCGCGANNAACGACGCCAGTCCGCTACGTNACCCCTCCGCAGTGTCCATGGACAAACAGCGCGTT
 CTCCACCGACCGGGCCCGGGTGTGGGTNTT (SEQ ID NO. 434)

:::::::Rv336T7.seq:::::::
 GCTGGTAGAGTCGCTGACCGGTGCAAGTTTCGACAATGTGGTGCCGGTCGGCGGCTACGTGCCATCGAGACACTGGC
 GCAGGCTATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTCTGAGCATGAGTCGGCAGCGTGTGTCAT
 GGTGACACCCACGACGGAAAGACGCAAGATCGCGTCAAGCATGTGTGCGCGGATTATCAGGACTGACCTCCTGGCT
 GACCGGCATGTTGGTCGCGATGCGTGGCG (SEQ ID NO. 435)

Clone Rv337

:::::::Rv337SP6.seq:::::::
 GCTTCCGCCGATACCCGCATGTCNCGCACATCCAGGACTCTGGGGGATCCGCTGACAGCGGGGATCCCAAAG
 TGCAGGATGATCGGGCCGCTACGTCGTGGTGTACCTCGTGTAAACAACGAAAGCGTATGACTCGTCCACGC
 GGTGCGGACATGGTGGACACCACACCGCCACCCGACGGGTGAAGGGCTATGTCACCGGTCCGGCANCACTCAATGC
 CGACCCAGGCCGAGGCCGGANACAAANTATCGTAAGGTCAACCGCGATCACNAGCATGGTATGCAAGCAATGTTGCT
 AGTGAATCTATCGCTCCGTAATT (SEQ ID NO. 436)

:::::::Rv337T7.seq:::::::
 CTTCAACCCGAATTGGCTTCGGGCCATCGGTAGGGACGGCGTGCAGGGTGCCTCAACGACGACGTCGTCGGGAC
 ACACCTCGATGCTGCCGATGGACCGGGTCGAACGCAAGCAGCTGATCGAGCTAACACGCCGGGAACGCTTCCG
 CGCGGGCGTGACCGCATCCGTTGACCGGGCGATCGGGTGTGATGACGGCATGCCACCGGAGCGACGGC
 CAAGGGCGCGTGCCANGTGCCCGGGCGACGGTGCAGCAAGGTGGTGTGGCGGCTGGCGTCCGATCGGCCCA
 (SEQ ID NO. 437)

Clone Rv338

:::::::Rv338SP6.seq:::::::
 TACTCAAGCTTCGCGAGATCCGGATGGCACTCACGCTGGACAAGACCTTCACAAATCTGAAATCTGACCCGATACT
 TGAACCTGGTCTCGTTCGCAATAACTCGTTCGGCGTGCAGGACGGCGAACAGTNCTCGGCATCAACCGTCCG
 ANCTGAATTGGCAGCAAGCGCGCTGCTGGCGCATGGTCAATCNACCGACGCTCAACCCGTA
 (SEQ ID NO. 438)

:::::::Rv338T7.seq:::::::
 CCCACGACTTCTCCTCGATCAGTTGGATTGTCAGAAGAGGCAACGAAAGCAGTGTGATCCTCGGGATGGTCAGCGCT
 ACATCGACCCGCCGTTACGCCGACAGCCTGCTAGATGCGCTGGCGAGCAGGTCCCACAGTTCGCCGCTAAGGCAC
 GGCGTCTGTTCCGTCGGATGCCATTGGCTCGCGTCTGCTCCATTGATCAATAGGGCTGGCAGCTCCGTC
 GGCAGGGCCTACGCCAACCCGTCACG (SEQ ID NO. 439)

Clone Rv339

:::::::Rv339SP6.seq:::::::
 CTCAAGCTTATGCGCGCCGGCCGAGGTCTGCTCACGGCAACCCCTGAAGTTAGGGACNACCTACTCAGCGAAAAT
 TTCGCTAATGTGAGTCCGGCCACCAAGGGGNANATCAACCCATGTCGATCATGATCACCCGGATACCGGATTGGCG
 TAGCGCCACGATCGTCNAATNTCCGCTGAATCATCGGATAGCTGATCCGGCGTCAACGCGTTTGANTCACCAC
 GCAACAGCGCCAGGCCGGCCGANCAGCGATCTCNTCGGGCGCATGGGCCCCAATCTNTCG
 (SEQ ID NO. 440)

:::::::Rv339T7.seq:::::::
 GTGTGTGGTGGAAACCCATCTGAGCAGTGTGCCAAACCGGGCAGACAGCTCCAATTGACGTGAGCCCGCTCACTTGC
 TGGGTAAGCGTC (SEQ ID NO. 441)

Clone Rv33

:::::::Rv33SP6.seq:::::::
 CTTTACACTTCTGCATCCGGCTCGTATGTTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATG
 ACCATGATTACGCCAAGCTATTAGTGACACTATAGAATACTCAAGCTGGCGTACGCCACCGGGCCACTCCG
 CACCATCTGTACCCGACCAAGATCTAC (SEQ ID NO. 442)

:::::::Rv33T7.seq:::::::
 CAGGCATGCAAGCTTCTAGCTGCCGAATGCGTCACCCCGATGCGCCAGATCGGGCTTCGCAGATAAAGCACGAACA
 GGCAGGCAAAACGTCNATCTCGGAGCCGGAAAGGGCAATCAGCCGACCGTCGACGAACGACACCAGCAGACCTTAG
 GCAGTGACGGCCGGCCGAAACATTACCGCCTCGTGATTAGCGTTCGTCCGCGGTATGCCGAGCAGCTTG
 CGGCAGATCTGAACGCTGTCTGTCCGGCAGCGGCACGGCGATCCG (SEQ ID NO. 443)

Clone Rv340

:::::::Rv340SP6.seq:::::::
 CNCAAGCTTGGGATGTTACCCCTGACAGCCTGAACATGTCNAAACACACGGCACCGAACGGTGTGGGGACCCC
 ATCGANTTCGAGTCGCTGGCGGCCACTTATGGCTGGTAAAGGCCAGGGCNANAGCCGTGCGCATTGGGTCGGTC
 AAAACCAACATCGGCCACCTGGAGGCGGCCGGTGTGGCTGGATNCATCAAGGCGGTGCTGGCGTGCAACGTGGG
 CACATTCCCCGCAACTTGCACCTCACCCGGTGGAACCCGGCATTACGCGTCGGCNACCGGCTGTTCGTGCNACC
 NAAAACCCCCCGTGGCGCCGGC (SEQ ID NO. 444)

:::::::Rv340T7.seq:::::::
 GGAAACCGGTAACCAAGATCAGCTCGTGCACCTCACTGCCGGGGTGAATTCCCCACCGGTGCTGCGCGTGCCTAG
 TGCACTTCTTGACGCCCTGAAAAGGGGAGTCGGCTGGTAGGTACCGTCAGGAGCCGCTACCCAGGTTGGCGCNA
 TAGCCGGTCTCTCGAGTATCTCCGCACCGCCCCCACCGGTGCGGTCTCACCCANATCCACTTGCCTGGCAGC
 GACCAGTCGTCGTANCNGGGCGGTGAATGACAACGATCTCGACCGGCCCTTCN (SEQ ID NO. 445)

Clone Rv341

:::::::Rv341SP6.seq:::::::
 TACTCAAGCTTCAAGAACAGGCCTGTTGTGGGCNACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGC
 GCACCGCCGGCATCTCCGGTCACGCAGGGCCGCGCCGCGCAGCGACGGCGTGTTCGCGCAGTTGCCGTCAA
 TGATGCTGACCTGATGCCAACCGGGCTCTCGCGTCTCGCGTTCACTAATCGCGGTGCTCAGCAGCGTCTCGA
 CAGCCACCACCGAGTGGCGACAGCTG (SEQ ID NO. 446)

:::::::Rv341T7.seq:::::::
 TAATGTCCTGCCAACGTCAACCAATCGCGATGAATTCAATCATGCCGCCAGGGCGGCCAACCAATGGTGGCGC
 AGCGGCAGCTCGATCGCAGCGCGAGGTTGCCGCCAGTTGATTCAACAGGGTAGGTATAGGCGGGCAGG
 ATAGTGACGAAGGCAAGACCTATATCTGCCGTCCAAGAAGAATCGAGTAGCGGTGACACAACGGAAGCG
 AAGTGTCGGCGTGGCG (SEQ ID NO. 447)

Clone Rv343

:::::::Rv343SP6.seq:::::::
 TACTCAAGCTTCTGTCAGTTCTCGGCCAGCAGACCAACAAAGAGCATCGGACATACGGAGTCACACTACCCGG
 CGGCAGTTCTGCCGCCGCTGACGCCAGCAGCAGCACATTACGCANATGCCAGCGCGTGCCTGG
 CACCGAGGTTGGTGTCTGGCGGCTACTCCAGGGTGCAGCGTGTACGACATCGTACCGCCGCA
 CCGTTCACGCAGCGTTGCCGCCAGCGGANNATCACATGCCGCGATGCCCTGTC (SEQ ID NO. 448)

:::::::Rv343T7.seq:::::::
 CCACCCGTGTAATTGGGATGGGCNAAAAGGCNAAGCACCGCGTGGCCAGAACGCCGGAGGGACAATCTGGGCG
 CTAGGGCTTCTCGCGGGAGGCCGAAACGTACGGCTTCAACACGTCGCGTCCGCCCTCCGACCGCGAACATT
 CGGGATGGCAGCAACCTGGTAGCAGCAGCGTGGCGGCGATGATCTGCAGCGTCCGCCGCGGTAGTC
 GCGCCGCCGGCGGCTACAGTCTGAAACCGCGATGACCATCGATGTTGGATGCAGCATCCGACG (SEQ ID NO. 449)

Clone Rv344

:::::::::::Rv344SP6.seq::::::::::

TCAAGCTTCTAGCTGCCGAATCCGTCANCCGATGCNCAGATCGGGCTTCGCANATAAGCACNAACAGGCCGG
 AAAACGTCNATCTCGGAGCCGGAAAGGGCAATCANCACCGTCNACAAACGACACCCGGCANACCACTTAGCAGTGA
 CGGCCGGCCCGAACATTACNCGCTCGTGTAGGCCTCGTCTGTCGGTCAATGCCGAGCAGCTTGCAGCANA
 TCTGAACGCTGTCCCTGTCCGGCAGCGCGCCGGCGTTGGGTGCCTGCCGAATGTGACNAACGGAGCCGGACCN
 TCTCGGC (SEQ ID NO. 450)

:::::::::::Rv344T7.seq::::::::::

CCGGGGCCACTCCGACAACTCNGTACCCNNACCAANATCTACACCATCGAATACGACGGCGTCGCCGANTTCGCGGT
 ACCCGCTCAACTTGTGTGACCCCTAACGCCATTGCCGGCACCTACTACGTGCACTCCAACCTACTCATCCTGACGC
 CGGAACAAATNGACGNTCGGTTCCGCTGACCAATACGGTCGGTCCC (SEQ ID NO. 451)

Clone Rv346

:::::::::::Rv346SP6.seq::::::::::

NCTGGCCTTGGTCCACACTAANACAATACTCAAGCTTCCGGCCGAGAGCCGCCAACTCACGATATCGTTAACGAT
 ATCCCGAGCCGATAGCTGGGGCTCGGTGGTGGCCAGCGCGCTGCACNAAAGGTGTGACCGTCATGAAACAGAC
 ACCACCGCGCCGCGTCCGGCGTCACTGCTCGANATCTCAGCATCCGAGCCGGTGTGATCGCCTTCGGCGTG
 TNGTGGGTCNCCGCCCCGAGCCCGAAAGGCCGGCACACAACCCCGAAC (SEQ ID NO. 452)

:::::::::::Rv346T7.seq::::::::::

CATCTGCCCACACACGGGACCGCGGTGGGACGGCGCTGACGCCCTGGTGGTCAGCATCGTGGCGGTCTGCTGTTG
 TATGCCAGCTTCCGCCGCAACTGCTGGTGGCGGTGGTGGCTACGGCTCGCATTGCTGGCTGGTGTGACCCAC
 CGCGCGACACCCGGTGGGCTGGGCTACGGCTGCTATTCCGGCTGGTGTGACGTCCTGTTGACGTCCTGTTGCCGTGG
 ATCGCGGAGCTGGTGGGCCCCGGGCGTGGTGGCACT (SEQ ID NO. 453)

Clone Rv347

:::::::::::Rv347SP6.seq::::::::::

GACAATACTCAAGCTTGACTGGCCACCCACCGCATGACCACCGACAGGGCCGACTGGTCTACACTCGAACGCCGG
 GGTGTTGATGCTCCAGCCGCTGAANTCGCTCTGCCGCGCAGGGCGTCNAACAGGTACAGGGCGGGGAATTGGCACC
 ACCACTTGGAAATTGGACCTTGATGTCACGGCCCATCGACGGCGACGGCACCTGCAAGGTACTCCACCGGAAGCCCG
 CGGGAAAATGCCCGCGTCCGTGCCACCGACGGCGCCANAAACCCGACACTAGGGCCGCCNAACGGCCCC
 GACACACNANTCAGCGACATAACCGTACGGCCACNAACCTGTCAACA (SEQ ID NO. 454)

:::::::::::Rv347T7.seq::::::::::

CCTCCAACCTGGCGGGGAAGCGACNCAGCCTACCGAGCTGGAGTCCANGACGCCAGCGGGCGTCGGTCTGCGTC
 GTGGTGGCGCCGGGGTGGCGTTGGCTGGCAACGATCTCCACCCAGCGGTGGTTACCCACGATCTGGCATANACG
 CGGGCGAGGCCGGTGCATACCGTATTGCGTCATTGGGACGGGTTGTGCATTGGCTAGCTGGTTGCCACACCC
 GTCAGGGGTTGACGTTGGCGGGTCCGGCGGGCCANCACCGCTGTACCATGCCGCCAAGCCGACCTGCGGCC
 ACCAACTGCAGCACCACATGTCGCCGTCGCGCCGATCACATGG (SEQ ID NO. 455)

Clone Rv348

:::::::::::Rv348SP6.seq::::::::::

CTCAAGCTTTTGAGCGTCGCCGGCANCTTCGCCGGCAATTCTACTANCAGAGAANTCTGGCCGATACGGATCTG
 ACCGAANTCGCTGCCGGTCANCCACCCCTCATGGCGATGGGCCGACNATGGCGCTGGACCAGATCTGTGCCGTT
 GCCGACGGCGACGCCGGTAGGTGGTCAAGTCCGGTCTACGCTGGGCTTGGGACGGTCCGACGCTGGTCCGGTT
 GCGCCGNAAGCGCGGGTGGGTGCCATCAGGAATGCCCNCCGCCGGACTGACGGCAGTGGCGCG (SEQ ID NO. 456)

:::::::::::Rv348T7.seq::::::::::

CNCCAGCTTGATTGGTCTGGTGCATTGGCAGCTGCCGAGCCTGGCTACCTCAACTACGACGGACCGCAAACAAATT
 GCCGCCCTCGGATCCGAGTTGGTGGGTACGCCGAATGGAGCACCATTCTCGGTGAATCAGACTATTCTGAGTA
 CTTGATCATCCACTCTGCACACGACCTGCCGAACCCCGCGCGCCCTGGCACCTGGAGCAGCTGGCGCAACGTGTGAG
 CCAGATCCAGGCAGTGGCATGGTCCGGTGTGACCCGGCAAACGGGAAAC (SEQ ID NO. 457)

Clone Rv349

:::::::::::Rv349SP6.seq::::::::::

CAATACTCAAGCTTGACTGGCCGACCTTCGCCACCCACACCGTCAACGCCCGGAAGTCNACGTCGCCAGG
 CCATCGGCCCTCACGGATGGATTGGCATGGTCCGGACGTGGTGTGACGCCGTCGCCGACCGAACCTACCAGCAGG

CCTTCTACGCCCGCGATCTGCCGGAACCGTTGCTGGTGGGTGTTCCNACGCCGACATGCCCTGGACATGCCGC
TGGTCNACTTCTTCTCACGG (SEQ ID NO. 458)

:::::::::::Rv349T7.seq:::::::::::
TCGACGGTTGGCGGCCCTAAATGCACTGAGGTCGTCAATTGACCCACAGCGGAAATGCCGACTATTGCAGGCCTC
CTTCGCCCTGGCTGCCGGAGAGGGGCTCCGCCGGAACCGCATGCAGGTATATGACCTCGGTTCTCGGGTGTACCGC
GTGCCTGTNTANGATNANCTCGCGTTGGAATTGTCAGCCGGCCATTACATCGAGCGCANATTGTACACNTGGC
CGGCCGGCAGACATACGCTCACCGTGATCTGCTCCACACGGACCGCCCTGTCGGATCCTGTCACGGTAANGGAAC
TTACGTGGCACTCGG (SEQ ID NO. 459)

Clone Rv34

:::::::::::Rv34SP6.seq:::::::::::
GACCACGCCAGGCTAACGTGACGCTACCGAATACCCTNCTAGTGGTGCAGGCTCCGCTGGAAATGCCCTGTA
CCAACTCGCGCACCGGTGCCAG (SEQ ID NO. 460)

:::::::::::Rv34T7.seq:::::::::::
CGGCACCCGACCCCTTTGAGCCGTCCGCCGTGCCCGGTTGAACTGGCGACGAGGGACTGATCGTGTGGCAAAT
TGGTCGATGGCACGCTGCCGCGATCTGAAGGTCN (SEQ ID NO. 461)

Clone Rv350

:::::::::::Rv350SP6.seq:::::::::::
CTCAAGCTTGGCGTACCCGACTTCCGGAGGGACACCATGAGCACCGCCAGCCGAGCACGAGGCCAAACTCCGCCGA
CGCAGGCCGGTTGGACTTGTGCGTGGACAAGGGGTTAGCCGCCGAAGCAGTGACGTACATGGCGAAAGCAGTT
CGCCTGTCGACCGACGGNCNNACCGTGAGGCTAGGGAAAGCGAGGAGCACATGGCCGCCGACCCGCAATGTACACGCT
GCAAGCAAACCATCGAACCGGATGGCTATNCNTCACGCCCATGCCCGGT (SEQ ID NO. 462)

:::::::::::Rv350T7.seq:::::::::::
CATGTCGCGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGGGATCCCCAAAGTGGGATGATCGGGCCGCC
TACGTCGTTGTACCTCGGTACAACACGAAACCGAAGCGTATGACTCGGTCCACGGGTGGGCACATGGTGGAC
ACCACACCGCCACCGCACGGGTGAAGGCCTATGTCACCGGTCCGGCAGCACTCAATGCCGACCAGGCCGAGGCCGGGA
GACAAAAGTATCGTAAGGTACCCCGATCACGAGCATGGTGTACGCAAGT (SEQ ID NO. 463)

Clone Rv351

:::::::::::Rv351SP6.seq:::::::::::
ATACTCAAGCTTGGTACGGTGGCGGGCGTGTGCTGGCCGCGGTGCGCGGCTGCGGTCTGTTTACN
AGCTCGCGCTGCTGACACTGGCGCNAGCCTGAAACGGCGGGGATCGTGGCCACCTCCCTGATCGTGGGCTACA
TAGCCCGCGTGGGAGCAGGCGCTTGTGATCAAGCCGCTACTTGCACACGCCCATCGCGTTATGCCGTGGAGG
CGGTGCTGGGCATCATCGCG (SEQ ID NO. 464)

:::::::::::Rv351T7.seq:::::::::::
TGTCAGTCGTTTCAGATCTCNTTTTATGACATGACTGGAGATCTGCTAGATTGAGCTCTGTGAGCGTGGGTAC
CGGATTCAAGCCGGTCGGTACGCCCGGTGGTACCGGCTTGTGCGGAGTGTGCTCGGCTCGAGTTCGGCATCGCGCG
CGAAGTGCAGTCGCGCAGCAAGATCGCGGCCGTAATGCCCGATGACCGCGATGACCGCGATCCAGGCCGAGAAGCG
TTCCAACCAAGTGTGCTGGCGGCCATCCCGCGAAGTAGACCAAGTGCAGTGGTGC (SEQ ID NO. 465)

Clone Rv352

:::::::::::Rv352SP6.seq:::::::::::
CAATACTCAAGCTCAAAACAGGCCGTGTTGGCGCACCGGCTGCCGAGTTCTGCACGCCCTCAANTGCC
CCCGCACCGCCGGCATCTCCGGTACGCCAGGGCGCGGGCCGCCGACGGNGTGTGCGCAGTCGCCGT
CAATGATGCTGACCTGATGCCACCCGGCGTTCTGCCGTGTCNCGTTCAATGCCGTGCTC (SEQ ID NO. 466)

:::::::::::Rv352T7.seq:::::::::::

TACGCTGGCGCTGGAGGGAGCCANNTACAACATCCACGCCAATGCTTGGCCGACCGAGGATGACCC
GGACATCCTGCCGCCGAAGTACTGGAAAAGCTCACACCCGAGTTCGCGACCGGTGGTGGCTACCTGTGACCGA
GGAGTGTGCGCAGCAACCGCATCGGTGACGTCGTCGGTGGCAAGGTGCGAGTGTGCGCTGTTGGCAACGACGG
GCCAAGTGCAGCAACGCCGTGGTACAAGATGTTGCCGGCGGGAGATCACCGATCTGCCGTGCAA
AATTGCTG (SEQ ID NO. 467)

Clone Rv353

:::::::::::Rv353SP6.seq:::::::::::

GCTTTCCCGTCGTCNNCGCTAACCGCGTGAAGCCGAAGCGGNTGGTTACGACTCCCTGTTGTGATGGACCACT
 CTACCAACTGCCATGTTGGGACNCCGACCAGCCGATGCTGGAGGCTACACGGCCCTGGCGCTGGCACGCC
 GACCGANCGGCTGCNNNTGGCGCGTTGGTGAACGGCAATACCTACCGCAGCCCACCCGCTGGCAAANATCATCAC
 CACGCTCGACGTGGTAGCGCCGGTCAGCGATCCTCGGCATTGGAGCCGGTTGGTGTGAGCTGGAAACA

(SEQ ID NO. 468)

:::::::::::Rv353T7.seq:::::::::::

CNGCTTTAAATGGCCTTGACNTGGCGNGCCGGCCACCGGGGCCACTCCGACAACTGTACCCGACCAAGATCTAC
 ACCATCGAATACGACGGCGTCGCCGACTTCCGCGTACCCGCTAACCTTGTCGACCCCTAACGCCATTGCCGGC
 ACCTACTACGTGCACTCCAACACTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGT
 GGTCCCACGATGACCCAGTACTACATCATTGCAACGGAGAACCTGCCGCTGCTAGAGCCACTGCCATGGTGCCTGATC
 GTGGGGAAACCCACTGGCAACCTGGTTAACCAAATTGAAGGTGATTGTTAACCTGGCTACGGCAGCCGGCTAT
 G (SEQ ID NO. 469)

Clone Rv354

:::::::::::Rv354SP6.seq:::::::::::

CTCAAGCTTGGCGGGAGGGTGCATGGCGACTCGGATTTACCCACCAAGGGCGCCAACGCGGTGTCCGCGCCGTCA
 GCTGAACGTTGCTGCCCGCTGGAGAACCTGGCGCTGCTGCCACCCCTGGCGCCATCGGACCTTCGAGGACCT
 GGATTTCGACGCCGTGGCCGACCTGGAGGTGGCGGTGGACGAGGTGTGACCCGGTTGATTGCTCGCTGGCCTGGCGA
 TGCCACCCCTGCCCTGGTGGTCATCCGCAAANACGAANTTGTGGTGGAGGCTCTGCTGCGACACCCACNA
 CGTGGTGGCACCGGGCAGCTTAGCTGGCAT (SEQ ID NO. 470)

:::::::::::Rv354T7.seq:::::::::::

CCGACGCCGTGGCCACCAACACCGCGACCGACCGTGACCCGGACCGGGTGCCCGCGAACCGGTCTGGCCA
 ATTGCGCGGGCACCAAGCCGTGCGCGCCATGGCGAACAGCACGCCATTGCCGAGCATCACACCCATCACCACCG
 TGGTAAGCCCGGCCAGCGCGCCGACGGAGATGATGCCGCTGCCAGTACACCCGGTTGGCTGGAACCGCGTGGCGA
 GATTTCGCGGGCCCGCGGGCCGGTACGGTCCGCACTGGGTGATGGAACCATGCCGACAGCACCCACCG

(SEQ ID NO. 471)

Clone Rv355

:::::::::::Rv355SP6.seq:::::::::::

TTNACTGGCCTTGGTCCACACTAGACAATACTCAAGCTTCCAGGACATCGTCATCGCGACCAAAACCGCAGCTAGG
 TCGGCATCCGGAAAGCATCGCAGACACCGTGGCGCCAGCGCCGCTGCCGGCAGGCCATTAGCCGGCAAATTAGCCC
 GCGCGGCTCCGGCTCCGANTACGGCGCCCGAATGGCGTACCGGCTGGTAACCACGCTTGCCTGGCGCTGGCGCG
 GCCTGCCGATCAGGTGGTAAATGCCGACA (SEQ ID NO. 472)

:::::::::::Rv355T7.seq:::::::::::

NGACGTCTTCCATCCGCGCGTGTGTTGGCGGGTTGGCCACAGCAGCCCGGTGACGGCGACGATGCTGGGCTGGT
 TGCGGCCCTGCCGACCGCGCTTGCATGCTGGTGGCTGCTTGGGACGATCCGAAATAGTCCACGCCGATCTGGT
 GATTTCGCGGGCTACCCCGGATTACCCCGCGCTCGACGAGTTTGGCTGGACTACCCCGGTGGCAATCTGCT
 GAACTCGCGCCGGTGGTGGCTGGATGTCGAGCGCCGTTACCTA (SEQ ID NO. 473)

Clone Rv356

:::::::::::Rv356SP6.seq:::::::::::

CTTCCTCCTGAGTACCNCCGTNTACTTGGATGGTAAAAGCGAATCNCGTTGGTCACGAACGCCGGAGGG
 ACAATCTCGGGCGCTGGGCCTCTCGCGGAANGCCGAATGTACGGTGTCTGACACTTCCNTCCCCCTCCG
 (SEQ ID NO. 474)

:::::::::::Rv356T7.seq:::::::::::

GAGCATCGGGACNTACGGAGTCACACTACCCGGCAACGGTATTCTGGCCGCCGCTGACGGCGAACGACGCCNG
 CGACCCACATTCACTGGCAGCGCGTGGCGGCCACGAGGTTGGTGTGCTGGCGCTACTCCAGGGTGCCTGGCG
 GATCNACATCGTCACCGCCGACCAACTGCCCGGCTGGGTTACGCAGCCGTTGCCGCCNCAGCGAACGATC
 CGCCGCGATCGCC (SEQ ID NO. 475)

Clone Rv357

:::::::::::Rv357SP6.seq:::::::::::

TACTCATGANCATCCTTAATCANNGCTTGCCTTTTATTAAATCTTGCACATTACTGCAAAGCAACAAACAAAAT
 CGCAAAGTCATCAAAAACCGCAAAGTTGTTAAAATAAGAGCANCACACTACAAAGGAGATAAGAAGAGCACATACCT

CAGTCACTTATTACTAGCGCTGCCGAGCGTGTAAACCGAGCATAGCGAGCGAACTGGCGAGGAAGCAAAGAAG
AACTGTTCTGTCAGATAGCTTACGCNCA (SEQ ID NO. 476)

Clone Rv358

:::::::::::Rv358SP6.seq:::::::::::
CTCAAGCTTCAGGTCAATGTGCNCCAAGCCCTGACGCTGGCCGACCAGGCCACCGCCGCCGGANACNTGCCAAGGCC
ACCGAATAACAACAACGCCGCCGAGGCGTTCGCANCCAGCTGGTACCGCCGAGCANANCCTCAAGACG
CTGCAATGACCAAGGCCTTACNCNCGCANCTCAGGCCAGAAGGCCGTCNAACGAAATGCGATGGTGTGACCANAAG
ATCAGGCCAGCGAACCAAGCTGCTCAGGCCNG (SEQ ID NO. 477)

:::::::::::Rv358T7.seq:::::::::::
CATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTATGCCGACTCTGGTCAGCTCGGANCCGCTGACACCCCGCT
AAGGCTGCTCAGCTCGGTGCTTACCTCACCGACGGCGAACCTCCCCCAGCTTACGACTATCCGGATGACGGCACCTG
GTTGCGGGCGAACCTCATCATCAGCTGGACGGCGCTACCGTCGATGGCACCCAGCGGGCGATGGCGGGCCCG
CGACCGATTCTGCTTCAACCTGTTGCGTGAACCTGGCACGTCATGTCGCGTGGCGTGGGACCGTGCCTGGGCGATTGAGGG
CTACTCCGGCGTCCGGATGGGTGTCGTCAGGCCAGCAC (SEQ ID NO. 478)

Clone Rv359

:::::::::::Rv359SP6.seq:::::::::::
TACTCAAGCTTGCAGGGTATCGCCTGGTCAACGGCACCGTATCGGATCGGATCGGATCGGATCGGATCGGATCGGAC
TTCGGCGAACNTCATCGCCTATGCCTCGCGGGGGTGACGCTGACCCGGGTGACNTGTTGGCTCGGCGGGCACGGTGC
ACCTGCACGCTCGTCTATCACCTCNGGCCACCGGAATCATTCCCGGCTGG (SEQ ID NO. 479)

:::::::::::Rv359T7.seq:::::::::::
GTTGGNGCCTCGTCGGCGAACAGTTCTCGCACGATTCCGGATTAGCGGACTGGTACCCAGTTGGTATGCGGGAAAG
GCGCTGACGTTCGCCCGCAGTTAGCTGTTGATGGACGCGGTGGTGTGATGTTCTGATCACGGAACCTGGCTGTAATAGCCC
AGGGTCGCCACGCCGTTCATCCGGGCCGGACCCGGCGCACCGAGCGTGTGCGCAGGTATGCGACGTGATTTCGCTG
AAGTCCCCGTACCCGGAGAACT (SEQ ID NO. 480)

Clone Rv35

:::::::::::Rv35SP6.seq:::::::::::
TGCTTCCGGCTCGTATGTTGTTGGAATTGTCAGCGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACG
CCAAGCTATTAGGTGACACTATAGAATACTCAAGCTCCAGGTCAATGTGCGCCAAGCCCTGACGCTGGCCGACCAGG
CCACCGCCGCCGGAGACGCTGCCTTGTCACCGAACAAACACGCCCGAGGCCAGCTGGTGAACCG
CCGAGCAGAGCGCTCGAACGACCTCAAGACGCTGCATGACCGAGCGCTTAGCGCCGCAAGCTCAGGCCAAGAACGCCGTC
AACGAAATGCGATGGTGTGCGGCATAAGATCGCCGAGCGAACAGCTGCTCAGCCAGCTCGAGCAGGCCAACGATG
ACGAGCA (SEQ ID NO. 481)

:::::::::::Rv35T7.seq:::::::::::
CAGGCATGCAAGCTTCCGGAGGGCAGACCCGTCATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTATGCCGACT
CTGGTCAGCTGGAGCGCTGACACCCCGCTAAGGCTGCTCAGCTGGTGCATTACCTCACCGACGGCGAACCTCCCC
AGCTTACGACTATCCGGATGACGGCACCTGGTGTGCGGGCAACTTCATCAGCAGCTGGACGGCGCTACCGTGC
ATGGCACCGGGGGCGATGGCGGGCCGGCACCGAATTGTCGTTCAACCTGTTGCGTGAACCTGGCACGTCATCG
TGGTCGGCGTGGGCACCGTGCCTGGCATTGAAGGCTACTCCGGCGTCCGGATGGGTGTCGTCATGCCA
(SEQ ID NO. 482)

Clone Rv360

:::::::::::Rv360SP6.seq:::::::::::
TACTCAAGCTTGGGTGGCGCTGTCGGTGTGCTTGGCGCGTGGTATCAACACCGCCACGAAATGGGGACA
AGAAGGATTCGCTGGAGCGGTGGCTGCTCAAACCTCACCGCCACCTGCTACGGGACTTCTACATCGAGCACA
ACCGTGGCCATCACGTCGGGTGTCCACACCGGAGGACCCGGCGTGGCGTGGCGTGGCNAACGTTGTGGANTCC
TGCCCCGCANTGTTATCGCGGCTTGC (SEQ ID NO. 483)

:::::::::::Rv360T7.seq:::::::::::
GGCCATGCCACCGCNCCGCCGGCAACGCTCAAAGGCACCTACTGGCACCAAGGCCACACGTACCCCTGTGACCTC
CTGCGCCGACCCCGCCGAGGTCTGGCGTACCGACCGAACGGCGAGGCCGGAGTCTGGTACGATCGAACAAAGA
GCAAGGTGCATGGCGAGGTGTTCCGCCACTTCGTCGATGACGGGCTGATCCATTGAGGTCCGTCGCCGCTCG
TCGAGTGGCGGTACACTCCANGTACTCGACCTCACAGACGAGGAGACTCGATCCCATCTAGGTGTGGACGAAACAGA
TCTTCTGTCCGACGACTACACCACCCAGGCCATCGC (SEQ ID NO. 484)

Clone Rv361

:::::::Rv361SP6.seq:::::::
 GCTTGCGGGTGATCGCTTGGTCAACGGCACCGTGATCGGATCGGGTCNACCGNCAGATGGACTGGANCTTCGGCG
 AANTCNTCGCTATGCTCGGGGGTGAACCTGACCCCGGTGACNTGTTGGCTCGGGCACGGTGCACNTGGTCNCCCTCAGGTG
 CGCTCGTCAAGCACCTCNGGCCACCGAATCATTCCGGCTGGCTGACACNACGGCACNTGGTCNCCCTCAGGTG
 AAGGGCTGGCNAACAAANGCAGACCGTCCGGACAACGGCACTCCCTTCCGTTGGCTTCCGGCGAATCCGGACG
 CCNAACCGACCGCG (SEQ ID NO. 485)

:::::::Rv361T7.seq:::::::
 GTTCTCGCACGATTTCGGATTAGCAGGGACTGGTCAACAGTGGGTATCGGGAAAGGCCTGACGTTGCCCGATT
 GCTGTTTGATGGACCGGGTGGTATGNTGATCACGGAACTGGCTGTAATANCCAGGGTCGCCNCGCTTCATCCG
 GGCCCGGACCCGGCGCACCGAGCGTGTGCGCAGGTATGCGACGTGATTTCGCTGAAGTCCCCGTACCCGGAGAACT
 CGAACACGCTGAGGCCTGTCACCGTGTGNNCCGGACCAAGCGCGCCAGCAACTGCGAAAATCGTTAAGANAGG
 TCGAATCGTTGAAATTGGCACCACCTGCACC (SEQ ID NO. 486)

Clone Rv363

:::::::Rv363SP6.seq:::::::
 CACAAGACAATACTCAAGCTTCAGGTCATGTGCNCCAAGCCCTGACGCTGGCGACCAGGCCACCGCCCGGANAC
 GCTGCCAAGGCCACCGAATACAACAACGCCGCCAGGGCTTCGCGAGCCAGCTGGTACCGCCGAGCANANCCTNAA
 AACCTCAAGACGCTGCATGACCAGGGCTTANGCCNCAGCTCAGGCAAGAAGGCCGTCGACAGAAATGCGATGGTG
 CTGAGCANAANATCGCCGANCGAACCAAGCTGCTAGCCAGCTCGAGCAG (SEQ ID NO. 487)

:::::::Rv363T7.seq:::::::
 CCACCCGTGCATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTATGCCGACTCTGGTCAGCTCGGAGCCGCTGA
 CACCCCGTAAGGCTGCTCAGCTCGGTGCAATTACCTCACCGACGGCGAACTCCCCAGCTTACGACTATCCGGATGA
 CGGCACCTGGTGCAGGGCAACTTCATCAGCAGCTGGACGGCGCTACCGTCGATGGCACCAGCGGGCGATGGC
 CGGGCCCGGCACCGATTGCTTCAACCTGTTGCGTGAACCTG (SEQ ID NO. 488)

Clone Rv364

:::::::Rv364SP6.seq:::::::
 GCTTTCGCCGATACCCNCCATGTCCGCACATCCAGGACTTCTGGGGGATCCGCTGACAGCGGGGGATCCAAAG
 TGCGGATGATCGGGCGCCTACGTCGTTGACCTCGNCGGAACAAACGAAACCGAANCCTGATGACTCNGTCCACGC
 GGTG (SEQ ID NO. 489)

:::::::Rv364T7.seq:::::::
 CAACCCGANTGGCTTCCGGCGCCNTCGGTGAGGACGGCGTGCAGGGTCAACGACGACGTCCGCGGGACACAC
 CTCGATGCTGCCGCATGGACCGCGTCAACGCAAGCAGCTGATCGATCTACNACGCCNGNGAACGCTTCNGCCG
 GGGCGTGACCGCNTCCCGTT (SEQ ID NO. 490)

Clone Rv365

:::::::Rv365SP6.seq:::::::
 GGGATGGGAAAGCGAAGCACCGCGTGGCACGAAACGCCGGAGGGACAATCTCGGGCGGCTAGGGCTTCTCGCG
 GGAAGGCCGAACTGATCGGCTTCAACACGTCGCGTCCGACCGCGAACATTGGGGATGGCAGCAACCTGG
 TAGCACCCCTGGCCGGCGATGATCTGCCAGCGTCCCGCGGGTAGTCGCCGCCCCGGCG (SEQ ID NO. 491)

:::::::Rv365T7.seq:::::::
 CAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGGTGATTCTTGGCCGCCGCTGACGG
 GCGAACGACGCCAGCGACCAATTCAAGCAGATGCCAGCGTGCCTGGCCACGAGGTTGGTCTCGGCCGCTACTCC
 CACGGTT (SEQ ID NO. 492)

Clone Rv366

:::::::Rv366SP6.seq:::::::
 CTCAGCTTGAATGGCCACCCACCGCATGACCAACCGACAGGCCGACTGGTCGTACCAACTCGAACGCCGGGTGTT
 GA (SEQ ID NO. 493)

:::::::Rv366T7.seq:::::::
 TTGGTGCAGGGAAATGGCGAGTCCCATTANTCGCTGATTGTTGAACAGCGACGAAACCGGTGTTGAAAATGTCGCC
 TGGGTGGGGATTCCCTCTCAAGCAAGAGTAACGGCCCCAAATAAGTTACTCGTCGTTGCAAAGACCGCTACC

CGATGCCATTATGTGTTCTTACGCTCNNNTCCGGTGCACCATCATTATCTGCACCTTGACTGCACATTGAG
 CTTAGCAGCGCTCG (SEQ ID NO. 494)

Clone Rv367

:::::::::::Rv367T7.seq:::::::::::
 GAATTNGCTTCGGCAGCATCGGCCAGGACCGCGTGGGGTGCCTCAACGACGACGTCTCCGGGACACACCTCGA
 TGCTGCCGCCATGGACGCCGCTGAACGCAAGCAGCTGATCGAGCTACAACGCCGCCGAAACGCTCCGCCGCCG
 TGACCGCATCCCGTTGACGGGGCGGATCGCGTGTGATCGTCGATGACGGCATGCCACCCGAGCGACGGCCAAGGGCG
 GTGCCAGGTGCCGCCGGCGACGGTGGGACTGGCGTGGCGTCCCGATCGGCCAGACGACATCGTGGCAG
 ATTCGCCGGGTACGCCGATGAAGTGGTGT (SEQ ID NO. 495)

Clone Rv368

:::::::::::Rv368SP6.seq:::::::::::
 TAAAGCTTCGTCAGTTCATNGNGCCCCGGACCAACAAAAGCATCGGGACATACGGAGTCAACTACCCGGCAACGG
 TGATTTCTTGGGCCGCTGACGGCGNAACGACGCCAGCGACCCATTCAAGCAGATGGCCAGCGCGTGCCTGGG
 GAGGTTGGTGTGCGCGCTACTCCCAAGGGTGCGCCGTGATCNACATCGTCACGCCGACCAACTGCCGGCCTCGG
 GTTCACGCAAGCGTTGCCGCCGAGCGATCACNTGCCGATGCCCTGTTGGGAATCCCTCGGGCGC
 TGGCGGGCTGATGAGCGCCCTGACCCCTCAATTGGGTCAAANACCATCNACCTCTGCAACAACGGCAGCCGATTG
 TTCGGACGGCAACGGTGGCGANCACCT (SEQ ID NO. 496)

:::::::::::Rv368T7.seq:::::::::::

CCGGGAGGGACCATCNCGGCGGCTNCGGCTCTCCGGAAAGGTTCTANNGTNNNGCGTTTCNACNCTCCGTGCG
 CCTGCGACCGCCGAACATTGGGTATGGNNGCANCCGTNAGCATCCNGGCCGGC (SEQ ID NO. 497)

Clone Rv369

:::::::::::Rv369SP6.seq:::::::::::
 CTCAGCTTCGCATCAGTCATAGAACCGGTGCGCTCCCACCGAGTGGCTGGTCGCCTCCAGCAGCATCGT
 TACCGCGTTATCGGAAACTCNCGAACACCTGACCAACGCGCTTGTGATGCCCTGAATCGATGCCGTGCGTGG
 GCTCATCGATACCGAGTGTGTTTCCGACCACTCCAGTTGCCGTACGGCAGATTGACAAAGCGGTGAAGCCCAG
 CCAGAGCAGGACGATCACCNGCAACCGGGGATTGCGCG (SEQ ID NO. 498)

:::::::::::Rv369T7.seq:::::::::::

GCTTGGCAGCTGCGGCTGGCGCCCTNGAGCTTCTGATCTGGATCTCCGGACTCGAGATGCTACTTGCCGGCCG
 TGGACGTACCCATTGCGGGCGGGACCCAGCGCCCCAGGTGACCGAGTTGGCTGACGCTGACCGGCCGTCGG
 GGTCGACGCCGTAACGGTCAGCAGCTCCGANGTCCNNCTGATCCGACCGAGCTGCCAATGCCGGTGGCAGCCG
 ACGTGGATGTGCCGGGGCTAGATGCCGGGGAGCAGCAGGACCCGTACCGACGGTACCTTGCCGAGTTNG
 GCCTGCCGCAN (SEQ ID NO. 499)

Clone Rv36

:::::::::::Rv36SP6.seq:::::::::::
 GCTTCGGCTCGTATGTTGTGAGCGATAACAATTNCACACAGGAAACAGCTATGACCATGATTACGC
 CAAGCTATCTAGGTGACACTATAGAATACTCAAGCTTGAGCCATCGGGCTATCAGCTGGTTGATGTCCCG
 (SEQ ID NO. 500)

:::::::::::Rv36T7.seq:::::::::::

CAGGCATGCAAGCTTGTGCTATCACATCGACCAACCGCCGACGGCTCGGCAGAACGCCCTCGCATATGGGT
 CGACGACCAAGCGGGTCGGACTTCTGGCTGCCAGCGCTGCCGCGTACGACAAACAGCGCGGTGAAACCGACACTCC
 TTGTGATGTCCCACCTATCACCTCGGTACGCACCCAACTGACCCCTACCGGGCTAGCTCAGCCCCGATCTTCCAGAGC
 TCCGCCG (SEQ ID NO. 501)

Clone Rv370

:::::::::::Rv370SP6.seq:::::::::::
 GCTTTTGAGCGTCGCCGGGGCGGCTCCCGCAATTCTACTAGCGAGAAGTCTGGCCCGATACGGATCTGACCGA
 AGTCGCTGCCGTGCAAGCCCACCCCTCATGGCGATGGCGCCACNATGGCGCTGGACCGATCTGTGCCGCTTGC
 CGCGACGCCGTAGGTGGTCAATTCCGGTACCGCTTGGCCGAGCGTGGCGCTGGTGGCG (SEQ ID NO. 502)

:::::::Rv370T7.seq:::::::
 CGAN CCTGTTGACGGCTACCTGAATACCCCGATNCCACCGCCGCGGCGTTCGACGCCGACAGCTGGTACCCGACCG
 GCGACGTGCGGGTGGTCGACGGCAGTGGATGCACCGCATCGTGGACCGAGTCGGTCACTTGATCAAGTCGGTG
 GATACCGGGTCGGCGCCGGTGAATTGAAACGGTGTGCTCGGGCATCCGGACGTGGAGGGCGAGTCGTGCGGG
 T (SEQ ID NO. 503)

Clone Rv371

:::::::Rv371SP6.seq:::::::
 NAAGCTTGTACACCAAGTGTTCNACCAGNCGCTCCATCCGGCGAAGTGGATACTCCCAGCAGGTAGCAGGTGCC
 ACCACGCTGGTCA GTGCGCGT CAGTCGCTTGC GGCGT GCAGCAGCAGTCCGGAAATAGCTGCCCTGGCG
 (SEQ ID NO. 504)

:::::::Rv371T7.seq:::::::
 CGCTGGNCGCCGGCGTGGCTGCGGTAACCAATTACCAACACTTTGGTAGCCGAAAGCGGGCGTACAGCG
 AAATGGCACAGCCACCGCAGTCGCCGACATCCCGCAAGATGGCAGATTTCGTGCGGTGAGGCCGGGAAGGCCT
 AGCGTCATTGTTGCTGGCAAGGTTGTTGGGGCC (SEQ ID NO. 505)

Clone Rv373

:::::::Rv373SP6.seq:::::::
 CTCAGCTTCTCTGCCCTTGCGTTNCGGATNACATCCCGAGCGACTCGGCTTCGGCGTCGATGTCGAAGTTCTC
 GATCAGCTTCTGGATCGACTCCGCGCCCATGGCACCGGTGAAGTACTCGCCGTAGCGGTGACNAGTCGGTAGAG
 GTTTCGTCNACNATCAGCTGCTTGGCGCCANCTGGTAAAGTGTCCAATGTCCTCCAACCGGTCCAGCTCACG
 CTGCGCGGGTACGGATCTGGCGATCTCGCGCTCGCCGCGTGCAGACTTGCGCCGCGCATCGGCCCTGGGGCC
 (SEQ ID NO. 506)

:::::::Rv373T7.seq:::::::
 GTTCACACCTACCTACTATGCCNAATTCCCGACACGGGTTGCATCAACACGGGATAAGGTTGAAATCGCTGGGG
 TGAACTGCGGGCTGGTGCCTCGCTGCAATCCCGGGAACCGCGTGTGATCGGATTCTCGTTGCCGGAAAGACAA
 TCGGGATGCAAAGCCGGGAGCAATTCCNCCNACACCATTCTGGCCGTAAGAACCTGGAGATCGAACCCCGGGTT
 CGGAGCGTTGAAACCCAACGGTTCTGCCGTTGGCGCANACCAACTACGCCATACCAAAT (SEQ ID NO. 507)

Clone Rv374

:::::::Rv374SP6.seq:::::::
 CTCAGCTTACGCCGACGCCGGCTACACAACACCAAGGAAACGATTGCCACTGCCGAAATCGGGAACGGTCTCG
 CACACCTGGTCTGTTGGGAATTACTCGGACACCAACGTCAGAACACTACGACGGCAGTGGACAGAATACGGC
 TCCCTGGTGGCGCCCCGATCGAGTTGGGAAGCTGATATGTGCTCTGGACCC (SEQ ID NO. 508)

:::::::Rv374T7.seq:::::::
 TCCNCATGGGATAACGGGTTAGATTCNACACGGCACCGTGTTCACAAAGCCGGTCAGCTGGCGGGCG
 ACAACGGTATCTACTTCACCCGTTCGCCGTACAAGAAAACCACTAGGCCACCATCGAGTCAAGAACACCACC
 TGGTCCGCAAGTACGCCGTACTACCGCTATGACACCGCCGAGGAACCGCCGTGCTCAACCGATGTGGAGCTGG
 TCAACGACCGCCTCAACTACCTCACCCGACCATCAAACCGATC (SEQ ID NO. 509)

Clone Rv375

:::::::Rv375SP6.seq:::::::
 CTCAAGCTTGGGTGTTGCCGATCACCGGAAGCCNACATGATCAGCCACGTTCGCGCCGCCGCATACGGCGCGTAC
 CGATCTCCGCGTCAACACCCGCGGTAATCGCCGACGGTGCCTGCGAGGCCAAGGTGACAACGCTGATTGAAT
 CNAGTTCCANGTCCAGCGGGT (SEQ ID NO. 510)

:::::::Rv375T7.seq:::::::
 TNAACAGCTCGCGGAGCCCACGACCTGCTGCGTGGATTGCCGGCGGGAGATCAATTCCAGGCAGCTCCGGACAA
 TGGCGCTCTGCTGGCCCGAACGAANGACTCGAGGTCAACCCGGTGCCTGGTGCACCTGCCGATCGCACA
 GGTGGCCCAACCGGGCGCTTGTGNNNGTGGCAAGCCGGCAGTNGCAAACCCAGCGTGTACANGCTCGGCT
 CGCAGTTGGCGAANAAGTGGCTGCCGTGATCACCTACCACCGCCANGATCTGGGTGTCA
 (SEQ ID NO. 511)

Clone Rv376

:::::::Rv376SP6.seq:::::::
 GCCANCCGGCTTGGCGTCGACTCCGTTCNGCACATCATACTGGTCCCCGGTACTGTCCAACGCGCCGGTGCCTAGC
 CAAACGTCAAGACTCTCAGTGTATCCAGTTCTGATCCGGCTGGCGCCGCTGCGCGGGGGCTNATNTACTTCGG
 ACTNATTATCTCATCAAAGGACACCGGGCGGTGGCTGAAATCCCATGGTGCGATCGGACACAN
 (SEQ ID NO. 512)

:::::::Rv376T7.seq:::::::
 CCGACCTGGTATCTTCCGATAGCGCGCGTTGATATCCGGTCTGATCTCTGCCCTAACGCCGGATCTCAGCAGGTCC
 CCATGCAAAGATCCGAGGTGTCCCNGATCTAGGGGTCTCGCTCCAGATGATGGAGCAAGTCGGCCC
 (SEQ ID NO. 513)

Clone Rv377

:::::::Rv377SP6.seq:::::::
 CTCAAAGCTTCCGCTCAGGCCGCTGCCGTAACGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGC
 GGCTACGTGCCATCAAGACACTGGCGCAGGCTATCGCACCCGTTATCGCTACAAACAAATCGCGGTATGC
 (SEQ ID NO. 514)

:::::::Rv377T7.seq:::::::
 CATCACCTGNTTATGAACTGGAAGCACCGCAGCGCTTCCCTTTGGCGAACATGAGCCAGCCTCTCGTGGCGGT
 CGGGTGCAGGTGCTGGCAGCTGGCCGACAGCCGCTGACCCCTGAAACCAGCTTCATATCCCGCACGAAACGA
 CGCCAGTCCGCTACGTAACCCCTCCGCACTGTCCATGGACAACAGCGGTTCTCACCGACCGGGCCGGTGGG
 GTGT (SEQ ID NO. 515)

Clone Rv378

:::::::Rv378SP6.seq:::::::
 AGCTTAGCTTCCGCCCGCAATAGGGCTCCAGCTCATCCGGTGTGACCAAGATAGGGGCCAGGGTGTACCGCTGT
 CTTTGCCTTGGCTGTCCGATGCGCAGCTGGCCCTCAGCATCTGCAGGTCCGGACAGTCGTTGAAAATGG
 TATAGCCGATGATGACCG (SEQ ID NO. 516)

:::::::Rv378T7.seq:::::::
 CCNGAACAGAAGCGGNGGTTCTACCGCGGTGTGCGGCCGGCGCATATCGGCTTTACTAACCGAACCCGATGTG
 GGCTCCGATCCGGCGCATGGCATCGACGGCGACGCCGATCGATGCCGAGGCTTACCCACCTT
 (SEQ ID NO. 517)

Clone Rv379

:::::::Rv379SP6.seq:::::::
 CTCAAAGCTTGGCGACTCGACAAGCATTCTGACAGTTGGCTCGGCATGGTAGCCAAGGTTCTGGTCCCA
 CCAGATCATCTGGTCCGGTAGCGCTCGTCCGGTATGCTGCCGCCGGATTCTCGCTGTATTACTCCCCCGAAGA
 ACGCCACCGGTCCAGCGC (SEQ ID NO. 518)

:::::::Rv379T7.seq:::::::
 GCNAGGGGGTATAGCTTCCGTCGACCGGCACCGCCAGCCAGAGCTGTTCCAGTGTGCTGGGATTCTC
 ACGGCTGCTGAGTGCCTGCCAGACCGCTTCCGCTCGGTTACAACGAGCCGGGGCTACGATCGTGCACGCTG
 AAGTTGGTGTCTCCATGGACTTGGGATGT (SEQ ID NO. 519)

Clone Rv37

:::::::Rv37SP6.seq:::::::
 GTGTGGAACCGTGAGCGATAACAATTTCACACAGGAAACAGCTNTGACCTTGATTACGCCAACGCTATTAGGTGAGG
 CTATATTAATACTCAAGATTGCGGTGAGCACATCGGCCAAGAACCGCCGAAGGCACGGCGAACGCCCTGCC
 TGGGGCGACGACCAGCGGGCGGACTCTGGCTGTCCAGGCCGATCGCGCGTCCGA
 (SEQ ID NO. 520)

:::::::Rv37T7.seq:::::::
 CACTGTCAGTACATATGCGCCGCTCTCCTCATCGCTGCGCTCGGCATCGTGCCTGGCATGGCTCACCC
 CAAGCCGAACCGGAAACGAGAACGCTGTTCCATTAGGGTGTGACGACCAATACAGATTGCTCACCAAGGAACTCAC
 GCAGCACCGGGACGGATGTCAGCCACCGCCCATCTGGGGTGGTAGCGGGGGAAATACGGCTAACGCCGCTCCGGTGC
 CGGCAGGCCAGCGCAGACCCCTCGGGCGGGACACGGCAACAAACGACGACCCATAGTTGTTCTTGCCGGATGGCC
 GTTGTGGACATATCGGGCGGGCGGGCGCCGAGGTAGTGGCTGAGGCCATCTCGTGCCTGCCGAATGGCC
 CCAGCCAAACCGTGT (SEQ ID NO. 521)

Clone Rv381

:::::::Rv381SP6.seq:::::::
 CTCAAGCTTACGGTGATCGCATCACCTGGTCATGAACCTGGAAAGCAGCGCAGCGCTCCTTTGGCCGCAACA
 TGAGCCANCTCTCGTCGGCGTGGGTGCAGGTGCTCGGGCAGCTCGGCCGACAGCCGCTGACCCCTGAAACCAG
 CTTCCATATCCCGACNAACGAC (SEQ ID NO. 522)

:::::::Rv381T7.seq:::::::

CTCAGAAGCCGCTAGCTGGTAGAGTCGCTGACCGGTGCACGTGGGNCAATGTGCGCTGCCGGTTCGCG
 (SEQ ID NO. 523)

Clone Rv382

:::::::Rv382SP6.seq:::::::
 CTCAAGCTTGCCTCATCAAGCGCAACAGCAGGGCGTCGGCTGGTCGCCATGACGGGTGACGGGACCAATGACGCA
 CCCGCGCTCGCGCAAGCCGATGTCGGGTGGCNATNAATACCGCACCCAGGCGGCCGGAAAGCCGGAACATGGTC
 NATCTCCACTCC (SEQ ID NO. 524)

:::::::Rv382T7.seq:::::::

ACTTCTATTCGACTGGTAGCTGCGCAGTCGACTGCCGGCTGGTCAAGGCCGGCAGTTGTGGATNCCACA
 GGCAC (SEQ ID NO. 525)

Clone Rv383

:::::::Rv383SP6.seq:::::::
 GCTTGTGTATTCCGTGGCACTGTCAGACATATGCGCCGCTCCTCCTCATCGCTGCCTCGGCATCGTCGCCGGCGGT
 CATGGCGTCACCCCTACCCAAGCCGAAACCGAGAACGTGTTCCATTATTAGGGTGTGAGCACCAATACCAAGATT
 GCTCACCAGGAACTCAC (SEQ ID NO. 526)

:::::::Rv383T7.seq:::::::

CGATATTCGTCGGCCGCGTTGTCTGACTGGGTGCGT (SEQ ID NO. 527)

Clone Rv384

:::::::Rv384SP6.seq:::::::
 GACCTGGCCACCAAGCCGGACGCGACCGTCGAGGTGGCGATCCGGCTGGCGTCAAGGCAGACCAT
 GGTCCCGGGCACGGCCACCGCACTGGTAAGACTGCCCGCTGCCGCN (SEQ ID NO. 528)

:::::::Rv384T7.seq:::::::

CCGGAAGTCTAGGGGACGACCTACTCAGCGAAATGTCGCTAATGTGAGTCGCCCCACCAGGGCAGATCAACCCAT
 GTCGATGATGACCTACCCGGATACCGGATTGGCGGT (SEQ ID NO. 529)

Clone Rv385

:::::::Rv385SP6.seq:::::::
 AGCTTCAGTTCTCCACGACGCTTCCAAATGAATTCCCGATCCACAATCTGGTCAGATACAGGTGCCATAC
 CCCTTACTTCGGNAACGCTGGCGATTGGCCCTGCCGTG (SEQ ID NO. 530)

:::::::Rv385T7.seq:::::::

CCGCCTACGGGTGCGAACATGCATCCGAGACCGATGCTCGAGCGCGACCCACTGCCGATGGCGGAACCGGCTGG
 TTACCCGGGTGGCGGTGACC (SEQ ID NO. 531)

Clone Rv386

:::::::Rv386SP6.seq:::::::
 GCGGCTGGTTACGACTCCCTGTTGTGATGGACCACTTCTACCAACTGCCATGTTGGGGACGCCGACCGCCGATG
 CTGGAGGCCTACACGGCCCTTGGTGCCTGGCAGCGCAGCGCTGCAACTGGCGCCTGGTNACCGGCAAT
 ACCTACCGCAGCCGACCCCTGCTGGCAAAGATCATCACCAAGCTCGACGTGGTTAGCGCCGGTCAGCGATCCTCGGC
 ATTGGAGCCGGTTGGTTGAGCTGGAACACCGCCAGCTGGCTTCGAGTTGACCGGACTTCACTGACCGGTTCAN
 (SEQ ID NO. 532)

:::::::Rv386T7.seq:::::::

GCCTTCCGACAATCTGTACCCAGGACCTAAGGAACTTCCGCGACTTCCGCGGTACCG
 CTCAACTTTGTGTCGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCAAACACTTCACTCCTGACGCCGAA
 CAAATTGACCGAGCGGTCCGCTGACCANTNTGCGTCCACGATGACCCAGTACTACATCATTGACCGGAGAAC

CTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGAACCCACTGGGAACCTGGTTCAACCAAACCTGAAG
 GTGATTGTTAACCTGG (SEQ ID NO. 533)

Clone Rv387

:::::::Rv387T7.seq:::::::
 GCAGACCAACAAGATGCATCGGGATCATGCCGTCAACTACCCGGCAACGGTATTCTGGCCGCCGCCCAC
 (SEQ ID NO. 534)

Clone Rv388

:::::::Rv388SP6.seq:::::::
 CTCAGCTTGCCTAAAGAGACCTCGTCACCAAGCNGGACCGACCGTCNAGGTGGCGATCCGGCTTGGCGTCCACCCG
 CGTAAAGGCANACCANATGGTTCGCGGCACGGTCAACCTGCCACACGGCACTGGTAANACTGCCCGTGCAGGTATT
 GCGGTTGGTAAAAGGCCATGCTGCCGTTGCCGGGGGGGGATGTTGCGGAGTGACAATCTGATCGANAGGATT
 CAGGGCGGCTGGCTGGAATTGATGCCGATCGCAGACACGGATCAGATGCCAAAGTCGGTCNCATCGCTGGGTG
 CTGGT (SEQ ID NO. 535)

:::::::Rv388T7.seq:::::::

CCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCGGCTTGATGTCGGCGTTAGCGC
 CGGATTCCACACATCCCTTGCAGAAAGTCCGTTGGGTGCAATGATGAGCGCTTCTCCCCATCGAGATAGTGGAGCA
 ACGCAATCCGTGCGGTACGGTTCGGGTCTACTCGATGTCGCGACCTTGGCGTTGACACCATTTGTCATTGCGGC
 GAAAGTCGATCATCCGGTAAGCGCCTTATGACCGCCGCCTTGTGCCGGTGGTAATCCGGCATGCGCGTTGCGTC
 (SEQ ID NO. 536)

Clone Rv389

:::::::Rv389SP6.seq:::::::
 GGCGGCTGCGTCGGCGAGATGATGCCCGGTGCCACCCGATCCGTGCTCGGTCAAGCGCAACGTGCTTCCGGTCC
 GGCGACCAACCATGTCGATGCGGCAC (SEQ ID NO. 537)

:::::::Rv389T7.seq:::::::

GCAATGCCCTGGCGGTGCCGGGTTGTCAACCGGTGATCATCNCGGNGGGATGCTCATNCGGCGCATTCGTCAAT
 CGTTCGGTATGCCACCTTGACGATGTCCTTATGGACCGCCATGCCGATGCCCGCTNCTG
 (SEQ ID NO. 538)

Clone Rv38

:::::::Rv38SP6.seq:::::::
 CCGGCTCGTATGTTGAGCGGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCAAG
 CTATTTAGGTGACACTATAGAATACTCAAGCTTCCACATCGGTATGCCAAAGCATTGCGCCGTATCGATTTCGCGT
 GGCATGCCAAGGTGGACTCTTGTCTCAGCGACGAGATCCCGTGGTGGATCCGGCTGCCGGGGCTGCCGACCCCTG
 CATCTCGCGGCACCCGTGACCGAGATGGCGCGCCGAGGGCAGACGTCGCGGGGAGGCCACGCCACTGGCGATG
 GTGCTGGCCGCGTGTCCGACGTCGCCGACCCCGGCCGATCGACGAAACGGCCGCGTCCGTTCTGGACCTATGCC
 CACGTGCCGTCGGGGTCCACGTCGACGCGACCGAGACCGT (SEQ ID NO. 539)

:::::::Rv38T7.seq:::::::

CGCGTCCACCGCAGCGTGGAGATTGGCGGCCATTGCTCGTGGTGTAGCTGCTGTTGGCGCGTCGCCGTATTGTGCG
 GGCGAGCCTTGTGCGGGGGCGCTTCTACCCACGAGTCGGCACTTCCGCAACCGCCCAGCTGACCGCGATTACGGCG
 GCGCAACGGCCGCCGGAAGGGCGTCTCGCAAGCGCTTATCCTTCCGAGGTTCCAGATCCTCCGCTACGTGGGT
 GCTCATCGCGGGGGCCCGCCGAATGAGTACAGGTGAGGGTAACCGCTACAAATGAAGTGGTCAGTGTGCCAACTG
 TGAATGGTTGCCGGCTCGGGTACCCACGTCACATTCTGGCAAGGGGGGAGATTGGTCTCGTCCGCGTCTGGCCG
 GTGGCGGTTCCCGGTTGTCGCGTGGCGTGTACGTGGTGAAGTGTGCGTAACCTCTCAGTTGGGT
 (SEQ ID NO. 540)

Clone Rv390

:::::::Rv390SP6.seq:::::::
 CTCAGCTTGCCTGGATCTGGCGCTGAGCTGTTCTGGCAACATGCCGAGGGATGCCCTTCCACGCCGT
 CGGGGTGGCGTTGCAATTAGCTACCGATGGTGCCTGTCAGGCCGGGATACCCCGAGTGCCGGTAAACCATCT
 TGTGCTGCAAGTTGTCGCCGCTGATGGCGACCTTGTGCCGGTTGATCAGTACNATGACNAAGTCACCGCCATGACATTGG
 GGCGAACGTCGGCTTGTGCTGCCGCGCAGCAGGTTGGCCGCCGACGGCAAGGGGCCAACACCACGTC
 (SEQ ID NO. 541)

:::::::Rv390T7.seq:::::::
 TTTGGGATGGGCAAAAGCGAAGCNC CGTGCACGAACGCCGGGAGGGACAATCTCGGGCGCTAGGGCTTCTC
 GCGGGAAAGGCCGAACGTACGGCGTTCAACACGTCGCGTCCCGACCGCGAACATTGGGGATGGCAGCAACC
 TGGTAGCACCTGGCGGGCGATGATCTGCAGCGTCGCCGGGTAGTCGCCGCCGGCGCTACAGTCTGAAACGC
 GATGACCATCGATGTGTGATGCAGCATCCGACGCAACGGTTCCCTACACGGCGATATGTTGCCCTCGCGCCGGTG
 GACCGGGTGGTCTATCCCGA (SEQ ID NO. 542)

Clone Rv391

:::::::Rv391SP6.seq:::::::
 CTCAGGCTTCGTCATAAGACCATGGTGCCTTCTTCACCCGTCANAGTCGGGGCATCCGACCGGCTCGCATCG
 CATCATCCTCCACGACGGCGCTCATCAGCTGGGCATTCAATGTACTTGATACCCCGCCTGCGGGTAGGCCA
 CTGCNACAATTCAAAACACGGTGTACACGGTAATANTGTCNANATGGCTCTGATCAACCGTCNAAACCCGGTTTC
 (SEQ ID NO. 543)

:::::::Rv391T7.seq:::::::
 GAATTCTGCGTGCACCGCTATGGGTTGCGAGCAGCGCTGGCGCCGACACCCCACTGGCCCGGGTGTTCGCCCCG
 ACCCGGATCATGGTAGCGAAAAGGAGATTGCGCTGTTGCGATGCTGGGATTGCCACCGCGAGGCCATCGACCGATT
 CTCGCCACCGGGGTGCGAGAGGTGCGCAGTCCGCTCCGACGTCCTCCGACGATCCATCCGCTCCGCCGTGG
 GTGGCGGTAGCCGTCGATGAAATGCGTGC CGCTACCCACAAGGTGATTCTGTCGGTGTGCGAAGTGCCTTTC
 GCGATCGACTTCCGTTGACCTACCGGCTGGGCGTCTGCACAACACCCCGGTGAGGTGCTTTGCGAGTTGGC
 GGAATCCGTGCTCTGGTTACAGCCCCGAACTCGTCNCGGCGTGC (SEQ ID NO. 544)

Clone Rv392

:::::::Rv392SP6.seq:::::::
 GCAGTTGGGAATCGCTCTGCAGCAAACCAATTCTGCGCAGTTGAGAGGACTNTTGAAATGGACGGATCTACCT
 GCCCGCGCAGGAGCTGGACCGATTAGGCGTACNCCTCGCTGGACGACTCCGGGCACTCGATGACCCGACGGACG
 GCTCGCGGCACTGCTGCCGTTCANTGCNACCGCGCCGCAACTGGTATTGCGTGGACTGCGCTGATTCCACACCT
 CGACCGCCGAGCGCTGCCGCTGCTGCGGCCATGTCGGCATCTACCGCCGTCNGCTCGCCTTGATCAGACCATCGCC
 GCGGTCGTCACCACCGCGAATCTCTGTTGGGACTGAANAANGCCAAGTGGCGGGCAGCACTGGNCTCTT
 CGGTAACCTGCNGACCGCCATTGGACCGCTACCG (SEQ ID NO. 545)

:::::::Rv392T7.seq:::::::
 TTGATCTGGACGCTCTGAGACGGTATCGGGNCGAACCTGAATTGTCGGTAATGCCAGCGCAGAAAGCANGGTGGTG
 GCCGGGGCGGTGAANCGCGTCGGCGCACCGTCAAGTCGATGTTGCCGAATGGGATGTCGGCAGCG
 AAGCCGTAGTCGCTTGTCCGTAGGGCCANGGATGGGATGGGGGAAGGATCGTGGTGTCCGGGATGATAATGGGGCCG
 ATGCCGCCGGTGAAGTCCAGTGGATCGGAATTGGGAATCGTATGCGACGTTCAAGGCCAACAGGCCCTCCAAG
 TTGCTCGCCACNAGATGCCGTTGCGAAGTGGCCGACATGAGGGCCGGTGTCCACATTGCCGAATTGGCGACG
 CGGGTGTGGC (SEQ ID NO. 546)

Clone Rv393

:::::::Rv393SP6.seq:::::::
 CACGTAGGCGCCGTCCATAATNACTCCGCCCGCTTCGACATCCTCGTANCATGCTTGGCAGCGAGGTCAACCG
 GCGCTGCCCGTCNAGGAGCCGGTTTGGCGTGCAGCCACTGGCGACACCTCGGGGGTAAGCGAATCCGAGAGCAG
 GAGGACNAGGTACGAACTCGGCCAGCCGGTGTACCGCTCAGGGGGATGTCGCCGGTCCGCCACCCCGTACCGC
 CGATCGGACACCTGTATGACCGCCGGCGACNTCGACCTGGGTGACGCCGAAGGGTTTCAGGGCATCNACTCGCT
 GCCCTCGACCGCCCGGTTCAAGGGTACCGCCATCGTGGTCCCTCGCAACTCCGGTTACTACCGTAAACGCTACC
 G (SEQ ID NO. 547)

:::::::Rv393T7.seq:::::::
 CGGGGAACGGTCTCGCACACCTGGTCTGTTGCGGGAAATTACTCGGACANAAACGTCAAGAACTACGACGGCAG
 TNGGACAGAANACGGCTCCCTGGTGGCGCCCGATCGAGTTGGGAAGCTGATAATGTGCTCTGGACCCAAGCAAGGAC
 TGACATTGCCGGCCAGCGTCGACCTGGAAAAAGAAACGGTGATCACCGGCCGCTAGTGGACGGTGACGCCAGGGCG
 TGGCGGGCGCGTTCTGCGGGCTGCTGGACNCCTCGACGAGTTCACCGCCGGAGGTGTCGCGTCCGCCACCGGG
 CGAATTCCGGTTCTCGCCGCGCCCGGGATCTGGACCGCNGGCGCGCTGTT (SEQ ID NO. 548)

Clone Rv396

:::::::Rv396SP6.seq:::::::
 CTCAAGCTTGTCCGACAAGCGTCCCGGGCGGTCAAGCAAGCGAACGTCGGTTGCCACTGCGGGTCGATATTGCCG
 CCAGGG (SEQ ID NO. 549)

:::::::Rv396T7.seq:::::::

550 CGTCAGCACGGCGACGTCGCGNTACGCCGAGCAGTTACACAATCGCTCTGCAGCAAACCAATTCTGCGCGACGTTGAGAGGACTTCTGATTGGACTG (SEQ ID NO. 550)

Clone Rv39

:::::::::::Rv39SP6.seq:::::::::::
 CTGCATCCGGCTCGTATGTTGTGGAATTGTGAGCGATAACAATTTCACACAGGAAACAGCTATGACCATGATTAC
 GCCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTCGCGCAGCGGCGGGTTGACCCGGTACGCCGATAGC
 TGGCAATCTGGCATCGTGCATCANCATGTTGGGGGGTACCTCGCGGTGATCGAAATACCCGGTCTTATCCC
 ATTTCAGGATTTCGACGGTGCCCGCGCCGACCGTGAACAGATGTGACCCGGCCGGCTCACGGCCAGCAAGG
 CGTCGCGGGCAGCGATCGATTCTCGCGGCCATCCCGCCAGGCCAGGCCATGGGCGCCATGGGCGATCAGCACGCCAAACCGGTG (SEQ ID NO. 551)

:::::::::::Rv39T7.seq:::::::::::
 CCGACGCGCACTACGTGCTGGTGCACCCCGCACCAGCAGGCTACGCAGCTACCGCATCGTCATGGCG
 CTGTCACCGAGGAACCTGTCATGTCGAGCAGTACTGAACCGTTCGAGAAAGGCCAGCATGAACGTACCGTAT
 CCATTCCGACCATCCTCGGCCAACCGCGCCAGAAAGGTGTCGAGCCGATACCTTGGGTGCCGTCA
 TCAGCGACCTGGAGGCCAGCTATTGGCATTTCGAGCGCCTGATGGACCCGTTCTCCCCAGGTAAAGTTCGACCGCT
 TCGTGAACATCTACGTCAACGACGAAGACGTGCGTTCTCGCGGCCATGGCACCCGCGATCGTGAACGGTGA
 TCACCATCCTCCCCGCCGTGGCGGTGGTGAGCGGACACATGACACGATACTGACTCGTGTGCATGCCCTG (SEQ ID NO. 552)

Clone Rv3

:::::::::::Rv3SP6.seq:::::::::::
 TGCTTCCGGCTCGTATGTTGTGGAATTGTGAGCGATAACAATTTCACACAGGAAACAGCTATGACCATGATTAC
 CCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTCGCGGGAGGGTGCATGGCCACTCGGATTACCCACCAAG
 GGGGCCAACCGCGGTGTCGCCGCGCTGAGCTGAACGTTGCTGCCGCTGGAGAACCTGGCCTGCTGCGCACCTG
 GTCGGGCCATCGGCACCTTCGAGGACCTGGATTTCGACGCCGTTGGCGACCTGAGGTTGGCGTGGACGANGTGTG
 ACCCGGTTGATTGCTCGGCCCTTGCAGGATGCCACCCCTGCGCCTGGTGGTCATCCGCGAAAGACGAAGTTGTGGTG
 GAGGCTTCTGCTGCCGACACCCACGACGTGGTGGCACGGGAGCTTAGCTGGCATTCT (SEQ ID NO. 553)

:::::::::::Rv3T7.seq:::::::::::
 GAAAACACCGNCGCCGTCGTGGCCACCAAACACCGCAGCACCGTACCCGGACCAGGGTGCAGCGCGAACCGGTG
 TTGGCCAATTGCCGCCGACCAAGCCGTCGCCGCGCATGGCGAACAGCACGCCGATTGCCGAGCATAACACCATC
 ACCACCGTGGTAAGCCCGCCAGCGCGCCGACGGAGATGATGCCGTTGCCGAGTACACCCGTTGGCCTGGACCG
 GTGGCCAGATTGCCGCCGCGGGCGTACGGTCCGAGTTGGGTATGGAACCATGCCGACAGCACCCACCGAT
 ACCCGCAGTAGAGAAGGGTACGACCCCCCAGCGACGCGAGAAATCCCTCGAGGGACGTCTGTTGAGGACGCTTGGTC
 TCCCGCCATGGTGGCACGATGTCAAACCGATAAACCGGAAGAACACGATCGATGCCGCCAGCACCGCTA (SEQ ID NO. 554)

Clone Rv40

:::::::::::Rv40SP6.seq:::::::::::
 CCTGCTTCCGGCTCGTATGTTGTGGAATTGTGAGCGATAACAATTTCACACAGGAAACAGCTATGACCATGATTA
 CGCCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTCGCGGGCTGGCCTGGCCAAGAAATCGTCGACGC
 CGGCCCTCTGTGCAATGCCCTGGCGTCGCCGTTGACCGTGTCCCTCAGATGGACGACGCCGATGGCCGCGCTGCTGT
 TTTCGTCGAAGCGTCCCGTATGCCACCTTGACGATGTCCTCAGATGGACGACGCCGATGGCCGCGCTGCTGT
 TATCGGTCCATTCCGCAACGACTAGGGGTGTCCCCCGCCGGAGCTGATGCCGTCGAAATGGCACCCACCTCTCAG
 TGGGGTGGCCACCGTACGCAAAACCACTTCATCACCGCAGCCGCCGACCTTGCAGGATCCGAACGGATGCCGTC
 (SEQ ID NO. 555)

:::::::::::Rv40T7.seq:::::::::::
 TTGTTGCTGATGGCGCCGCCGGTACGGTTGACCTGTTGAGCTGCGAATTGGGGTCAAATTCCGAGGTGGCGCGCT
 AAGAGTGGTCATCCCTGCCGCCCCGGCGAACCTGCGCCGGCTCACCCGCCAACACCGGACCGAGCTGCTGTTGCA
 CGGCCCTGCCCTGGTATCCCGCGCGCATGACGAGCACGACGAATTGCCGAGCTGCTGGCTTCCCGCGGTGCGGAAGT
 GCTGTTGCTGCGGACCTGTTGACTGAGGCACATCACAGCGGGGCCGCGCATGCGAGGAGATGCCGCTGCCGT
 CGACGCACCGCGGCTGGGACTGCCGTCGCCGAAAGAATTTCGGCTACCTGCCGATCTCGACCCAAGGACGTTGGCG
 CATGTCGACGCCGGCATGACTTCACGAACTCCNTCCGACACGCCGAACGAGATGTCGTTGGTGCATGCG (SEQ ID NO. 556)

Clone Rv412

:::::::::::Rv412SP6.seq:::::::::::
 GCGGCAGTGTGGTGGTGCACACGAATCCAACGACGCACTGGCGGAGAGATACCACTGCTGTACTGGAAGCAC
 GTGCTGATGATCTCCCGTGGAAATGTCGCTGCCGCCGTATCGAAAACAGTGAGCATGCTGCG (SEQ ID NO. 557)

:::::::Rv412T7.seq:::::::
 CAACCGCGCTCGCGCGCTCTGGCCTTCCGCCGACAATTCTATCTGGATCAGCGGGCTCTCCGGGC
 CGGCCCTCCGCGAACCTAACAGGCCGCGCTTCCGGCGAACATTCCTAGCCATATATGATCGCACCTCGATACACG
 ATCTGGCGGCAACACCGCAAAGCGTCCGACGGGCCAACCTCCGCAATTCAAGGTATCCGGG
 (SEQ ID NO. 558)

Clone Rv413

:::::::Rv413SP6.seq:::::::
 GAAGGTCGGCGAAGGTGGCTGGNTGCCATCGAATCCAATGATGCAGTGGTCGAAGATATTAGCCACTTGCTG
 TTCTGGAGACAGGTGCTGATGATCTCCGTGGATGTCCTCGACTCCGTCTATGAAATCTGTGAACA
 (SEQ ID NO. 559)
 :::::::Rv413T7.seq:::::::
 TCCCTCGCTCTGGCCATTCTCGGGCTGCCGACAATTCTATCTGGATCTGTGGGCTCTCTGGCCGCCCTCNGC
 GATCTCTCANGGCCGCGCTTCCGGCGAACATTCCCATATGATCGCACCTCTATACACCGTTGGCGGC
 AACACCGCAAAGTGTCTGTCG (SEQ ID NO. 560)

Clone Rv414

:::::::Rv414SP6.seq:::::::
 AGCTTACGCTGGCGTATCGCGTGGGCCGCTGCCATTCTGGTCGCCAACGCCGTTGCCAGCTCCCTGCCGTGCA
 GGGCTGCGGCCAAACTGGCACCGAACAAACTGGCTGAGCTTGATC (SEQ ID NO. 561)
 :::::::Rv414T7.seq:::::::
 CTCTATCTGGCGTCACATTGCAATTTAGATTGCAAGATATGATAAAATCACCCGCGACAAGACCGCCATGTCA
 TCCCTTCGATGTTATTCGCCGGCTGGGAAAGCGAACGACGTTGCCCTACACGTTCCGCCG
 (SEQ ID NO. 562)

Clone Rv415

:::::::Rv415SP6.seq:::::::
 AGCTTNCCTTGCATCTGCACCCGATCCACGTCAGCCACGTGGCATTCTCC
 TGCCCTGGCGAGCTGCTGCCCTCGTAGGTGAACCAGGCCACCGACTTGCGGATGAGGCCCTGATCCACACCATGT
 CGATCAGCGAGCCCTCCCTGCTGATCCCTTGCGTAGAGGATGTCGAACCTGGCTCTGTTGAAGGGGGCGAACAGT
 TGTGCACGACAACCCCTTCGGCGACGAGGGTGTGAGTTCTGACCTCGAGGTGCAACGTTCTGCCCCGCCGTTG
 GCAGCACTTCTCGGATCACGGAATAGCGGANTTCTTCCGCCAGCATGTCGTGCAGGAATTGTCATCCAGGGCATCCG
 CGAGGCCCTGACGCG (SEQ ID NO. 563)
 :::::::Rv415T7.seq:::::::
 ACTGTCAGGAAATGCTTCGACGATCTACCTGCAGTCGCTTGTGCATAAGCGGACGGCCNACCTGTTGTTCCG
 GGACACCAGACGCCGGAGCACCGGAGTACCGGAAAGGTTGAGCGGAAGGAGTGCACGAAATCGGGGCCCAAC
 ACCCGTCCGCAAGACGCCGTCACGACCTGTTCAAGGACTCAGGGTCAACCGACTCACCTGACTGAGAACAGCGAT
 CTGCTGATCTGCCAGAAGATGGACATGAATGTCACGGCAAGCCTGATGCCCTGCCCTTCCGGAAATGTTGGC
 (SEQ ID NO. 564)

Clone Rv416

:::::::Rv416SP6.seq:::::::
 TGAATTATGATCCGACACAACACTGCATCANTTCTAGCCGCGTGNAGTCTATCCGCCGACGGTTGGANCNGGTCGG
 GTCGTTCTGTTGATCTCACCGAACGGTGTGTCGCCGCCGGGATCTAGCGAACGCTGGGATCGACAAATCAGCGC
 CGCCAACAAGGCCGAGCGGCTGCGACCGCAGGTGCTGCCGCCGATNAGGTGTCAGCGCGATCGCAG
 GCTGTTGGTATGTCAGGCCGATCAAGTGCCTGNAATATCCGGCGATCAGTGCACGTTGCCGCTTCCGGAAATGTTGGC
 (SEQ ID NO. 565)
 :::::::Rv416T7.seq:::::::
 AACGGGGACCNCAAGAAACCATTCANAACGAGGGGTCGTCAACCAACGTCGAAACCGACGGTTGCCAGCCGCCACG
 ATATTGCGTGCCTGAGGGTCCGCGTGTACCCCTCACCGAACGTCAGTCCACACCGCGAGGCGGGGACTCTGGCGTGC
 TTAGCAGCCGAGCTCAAGGTGTCCGACCAACTGTCGAAATGCTTAAACCGACCGGATCAGCTCTCCGCCATCTA
 CGTGAACGAGTGCTTGCACGCCAAGCGACTGGCTATGCCGACCGGATCCGGTGGCGATCGTTGCCGACCGC
 AAAGCCGGTGCCTG (SEQ ID NO. 566)

Clone Rv417

:::::::Rv417SP6.seq:::::::
 AGCTTTGGAGCCNCNCCGANCCNCGGTACGCCCCGCCACCGCCGTACCCGGCACCCCTTGAGCCGTTGCC
 GTGGCCGCGGGTGGANCTGGCCGACGAGGGACTGATCGTGTGGCAAAGTGGTCATGGCACGCTGGCCGCCATCTG
 AAGGTCGGCATGGAGATGGAGCTGACGACCATGCCGTGTTGCCGACNACGACGGTGTGCAGGCCATCGCTACGCG
 TGGCGGATCCCATCGCGCCGGCGACNATGCANAGCGCANCAGATGCTGAGGAGCGGCCGATGAGGATGAGCGC
 CGGAACCGTTACNTCCTGGGTATGCACCCGTGGGGAAATGGGTAATGACTTC

(SEQ ID NO. 567)

:::::::Rv417T7.seq:::::::
 TTCTCNCATCGTCGTACTNNGATGGGACGCTGCTGCCGAGGGCGATCTGGCAACCGGCTCTGCCGCCGCTGACC
 TTCCGGGGGCGAACCTGAACCTCTTCCGATGGCGCTTGGGCCAAACGTACCGGGCTATCTCATTGCCGTCAG
 ACGAAAGATATTCCCGTCTACCGCTTGTATTACGTGTTACGCCGCGAGCTGGTCAAACCATGTCAACCTCACC
 TGGTCGATCGAAGGGGGTCGGGACAGAACGGGCAAGCTACGCCACCCTGTTGGGATCTGCGTTACATACCGAT
 GCGGTCGACGAAATGACGGTCCCAGTGTATTGGTGCCACCTCGATCGTGTACGAACAGCTGCACGAAGTGGAA
 GCCATGACCACCGAACCTATGGCGCCGTGAA (SEQ ID NO. 568)

Clone Rv418

:::::::Rv418SP6.seq:::::::
 TTCTTCCGGGTACCGCTGATCGCGGCCACCATCACGCACCCGGTGCAGGGCGAGGCGGCCGCCGTGTGGTGTGCTA
 CGGCCGCCAGCCGGTACCGGTGTGATCGCCGGTGGTGCGCCGCCGCGCGTGGAAATGTGCGGGGGTGCACGAC
 ATCTTGGCCAAGTCGCTGGCAGTGAACACGCGATCAATGTGGTGCACGCCACCCTGGCGCGCTCAAGCTGCTGCAC
 CGTCCGGAGGAGGTGGCGCGCCGCCGGTTGCCAATAGAACGTCGCCCCCGGCCGGGATGCTG (SEQ ID NO. 569)

:::::::Rv418T7.seq:::::::
 GTCGAAAGTGACCATCTTACCTTGAGTGCCATACCGCCGACCCCTATGCCCTGGATAGCTCGCGGAAAGAACGCT
 TGCGAGTGCCTGCAATAGGCGGCTACGTCGTGAGCGCCCATCAACTCTCGCGGGAGTGCATGCCAGCTGGCGCG
 CCGACGTCGACCGTGGGGATTCCGGTGCGCCGCCGCAACGGCCGATCGCACCCGACGGCAGATCGCGCGA
 TGTTCGTAACGCTGCATAGGCACTCCCGCGCGCTGGCAGGGCAGTTGCCAAGCAGCCCCCGCCGGTGCCTCCGTCGG
 TTGGCTTACCGCAAATTGGGTTGCCCT (SEQ ID NO. 570)

Clone Rv419

:::::::Rv419SP6.seq:::::::
 AAAGCCACGAAACGATTGCCACTGCCGAATCGGGAACGGTCCCTGCCACACCTGGTCGTGTTGCCGGAAATTACTC
 GGACACCAAAACGTCAGAACACTACGACGGCAGTGGACAGAAATACGGCTCCCTGGTGGCGCCCGATCGAGTTGGGA
 AACTGATATGTGCTCTGGACCCAAGCAAGGACTGACATTGCCGCCAGCGTACCTGGAAAAA (SEQ ID NO. 571)

:::::::Rv419T7.seq:::::::
 TTTCGCCACCGCNAGGTGCGCGGTCCAGAAAAGCGTGGTTTCGCCGGCGAGGATTGACGGTCCAACGTGACC
 AGCCGGTCCGCCACCCGTTAGGCAGGATCGCGGTGTCTATATGTTGCCCTGGCATAAACGCCATTGCTCGGGTGA
 AAATCGGACATCTGCCGATTGCCACGTCTACATGATCCGTTGTCCCGCGCGGGTGTGACAAACCGGATGTCN
 GCCTCTGGGAAGCGGTGGC (SEQ ID NO. 572)

Clone Rv41

:::::::Rv41SP6.seq:::::::
 TCGCCAAGTGGATTGCTGCTCACCNACGAGATCGTGGTGGATCCGCGCTGCCGGCTGCCACCCCTGCATCTG
 CGGCCACCCGTGACCAAATGGCGCGCCGAAGCAGACGCTCGCGGGACGCCACGCCACTGGCGATGGTGTCTG
 CCGCGTGTCCCNCGTCNCCGACCCGGCCGATCNACCAAACCGGCCGCCGTCCGTTCTGGACCTATCCCACGTGCC
 NTCGGGGTCCACGCTCGACGCGACCGANAACGTAACCAGCGTCTCGANCGGTTGCCCGGGCTCCGTGACATCGT
 GGTGGCGGCCGCCGT (SEQ ID NO. 573)

:::::::Rv41T7.seq:::::::
 GTACCGTCACCATGATGCCCTCATGGCATCGGTGAGCTGATAGATCCAGCCGGTTGCCAACCCGGAGCGATC
 TTGGCGCGCTGCTNGTNGTCNTGANACNTAGCCACCAACAGAGCCGGTGTGCGACAAGANGACTGATGGATCTC
 CCGGACACNTCGAGGGGGTCNTCAGGAGNCCGGCGCACCCGAGGTAAGCCTCCGCCAGCCTCACACCGCGACCG
 GGTATCNCAAGTCGCGCAATAANCCACCACTCTCGGACCCACGTTGATGCCGCTGGG (SEQ ID NO. 574)

Clone Rv42

:::::::Rv42SP6.seq:::::::
 ATACTCAAGCTTAGACCTACTGATGGCGGGACCGCGGGAGATAACCGCGGTTGAGCCGTTCAACAGTGGTGGTTC
 CCACACCACTGTTGCCTTGCAGAAGTAAAGCGATTGCTGAAAGAGGGCTGGCTGCTCGTGAGGGACAT
 CCATGGCCGATACTCAGCGATCTCAACGGTCAAGCGACTGCACTGATGTTGGCGAAGGTATCGTAAGCATAGGTCGT
 GACGGATTGACAGCAAGAGCTTCAAAGATTGCTGTCACATANTGATTGCACTCTACACCTCTCGCCGGTGC
 TGTCAAGAGGCCATTGCAATCAGTTATCTGCTGCTGGAAANAAATTTCAGCCTGCGTTGGACAAACCGCGTC
 GCCAAAGCGGT (SEQ ID NO. 575)

:::::::Rv42T7.seq:::::::
 AGCTTCCCGAGAAACAGTGCATTCCCTAACGAGCCGTTGTCACGCCGATGAGTGAAGAGTGCACGCAATGCCGGAA
 TCCGGCAAGCCTGCAACAGCAGAAATCAACCCGGAGGCTGACAAGGCAACGTCGGTATCCGTACCGCTGGTTGGA
 CAAACGGCAGAAGCGGGCTCGTCCGGTCCATCTACGCCGAGCACACTGGTATAGCGCGCATCGGATCGTGC
 CACGGTGGAGACGACGTCCCGGGCTCTGGGTCAAGTAACCCGCCGACCAAGTCTCGGGCAAGCTGGTGCACCATCG
 GCGCCACGTCTCAAACGCCACGCCATACCTGGTGCCTGGCATCGGCGATCGGGTGTGCGCATTGGGCGGATCGGA
 CGTCGAGAACGAGCCACCCGTGAGAAGTGACCCACGGCGCTGGACACGTGCTGGTAC (SEQ ID NO. 576)

Clone Rv43

:::::::Rv43SP6.seq:::::::
 CGGGCGGGATGTGCGCAATGGCAGGTGTCGCCCGGCTTGATGTCGGCGTTAGCGCCGGATTCCACCACATCCCTTG
 CGAAAGTCCGTGGGTGCAATGATGTCGCTCTCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGTT
 CGGGTCGTAACGATGTCGCGGACCTTGGCGTTGACACCATTTGTCATGGCGGCGAAAGTCGATCATCCGTAAAGC
 GCGCTTATGACCGCCGCCTTGTGCCNGGTGGTAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGCAGCGGGCG
 CACCAAGCGACNTCTCCGGGGTTGACCGGGTGTACCTGGCGAAATCAGATAACGCTGGCGCCGCGACGACCAGGCGTGT
 GGGCTTGTACTTGCAATTGCCATGGTCTAATCAGGTCTTCTCACCTCTCGTCGCCGGCTAGGGCGCATTGCCT
 GCTCCT (SEQ ID NO. 577)

:::::::Rv43T7.seq:::::::
 TAGCGGTGTAACCAACTCCGGTCAACCACCGCAAACCTCTTGCACGACCGTCAACCGGGCTG
 CCCGAATCCTGTGGATGGCATCGAGTGCATGGTCACGACGCTCCCGACGCCGGTGGCAACGACAAGTGGCCCG
 GATGCACCACAAATGACGCCGCACACCGGTGGGACGCCAGCACGAGAGGCCGTGCGCCGAAGTCGACGCTAATGC
 CGTAGGCATTGGCGTCACAACAGGGACGCCCGTACCAACCGAGTCCACGGNGTTGGCGGTCTCTCGGCCAA
 CCAGCGTGAACCCGGGATCCGAATGCAAGAACCGTGGG (SEQ ID NO. 578)

Clone Rv44

:::::::Rv44-2ndSP6.seq:::::::
 CCATTGGTCGGTGTGCGCATAACANTACNACGCCGGGACCTGACGCCGGCCAAACCATCGGTGGCCATCGC
 CATCGTCTGCCACCCGGTCAACGGACGACCTCTCTGGCCACCTAGTGCACCCGCCGCGTGCCTCGACCAT
 CGATCCGGTCAACATGAGCAGCGCCACACCGAGCGGTACATGACATCTGCTGTGGAACCAAGTGCACANATTCCGCC
 CCATGATGATCCTGACCGTCTCCGGATCGGT (SEQ ID NO. 579)

:::::::Rv44-2ndT7.seq:::::::
 GCGGGCCTGGTCAAAGGGCGTCCGAAGGANCCGGCTGGGTAACAAGTTCTGGCTCATATCCGGAATGCGACGCC
 ATTGTCAGGTGGTGCAGGTTCTGCGACGACAGTGCACCGGACGGGTCGATCCCAGTCGACATT
 GAGGTCGTCGAGACCGAGCTGATCCTGGCAGATCTGCAAACCCCTGGAGCGGGCCACGGGGCTGGAGAANGAAGCN
 CGCACCAACAAGCGCGCAAGCCGGTACGACCCGGC (SEQ ID NO. 580)

Clone Rv45

:::::::Rv45SP6.seq:::::::
 GATCCACTGACCACGATGACATATCGAAATGCTCGACGATTCCGATGGCGATCAAGGCCACGATGCCCTGGCGTTGG
 CGGGTATCTGGTGGATGGTACCCGGTAGGTTCCCGTGTGTCGACCCAGTCCACGCCGATGGCGCGAGGT
 CGTCCGGCACCGCATACCCCGCGTNTGCCGCCAGTGCCTCGAGTTGGCGCAGCTCTCCCGTAGAAGTCTC
 ACCGTTGGTCGCCCGATCTCTANCGTCGCCGTGGTCAAGGAAAGTAAACAGCTACCGGGTTTCGGCGCTCG
 TCCGCCGGGATGAACGCACTGCGAATCCGGGCTGGGATGCGAACAAACGGACCTGTGCCG
 (SEQ ID NO. 581)

:::::::Rv45T7.seq:::::::

TCTACTGCCGAATCGGGGAACGGTCTCGCCCAACNGGTTGTTGCGGAAATTACTCAGGACACCAGTCGAG
 AACTACGAGCGGAGTTGGACANAATACCGCTCCNNGGTGGCGCCCATCGANTGGGAAGCNGAAATGTGCTCTGG
 ACCCCACCAAGAATGACATTGCCGCCCTCAACTGAAATAGAACNGTGTACACCCGCCGTTGGAAAG

GAATGGCATGCCCTGGGCCGGCGTCCCTCCGCTGCCGGACTCCTCCCACCAATTACCGCCGAAGGCCTCCGTCT
GC (SEQ ID NO. 582)

Clone Rv46

:::::::::::Rv46SP6.seq:::::::::::
ATACTCAAGCTCTGTACCGAAATCCGCATGGATAACGGGTTAGATTCGACAACGGGACCGTGTTCACACA
AGCCGGTCATCAGCTGGGCCGGCACAACGGTATCTACTCACCCGTTCGCCCGT (SEQ ID NO. 583)

:::::::::::Rv46T7.seq:::::::::::

CTGGCTCAAGCGCTGGCGCAGGTGAACCTGGACCGGCTCGACGTGCCGAACCGAGGGCGGTGCTGGCCACGCC
GACGCCGTCGCGACATATCGCACCGTGCACAAGTCTACAACAACGCCGGCATCGTACAACGGCAACGTGACA
AGTCGGAATTCAAGGACATCGAGCGCATCATCGACGTCACTCTGGGGCTCCTCACGGGCC
(SEQ ID NO. 584)

Clone Rv47

:::::::::::Rv47SP6.seq:::::::::::
CCGCCCTCCGATTATGGGTCAAGAACCATCGGCTGGACTTCTGGGTTCCAACGCTCGCCCGTCCN
(SEQ ID NO. 585)

:::::::::::Rv47T7.seq:::::::::::

CCGTGGCACTGTCAAGACATATGCCGCTCCTCATCGCTGCCCTGGCAGCTCCAGCAAAACCCGCTCCACCC
CTACCCAAGCCGAAACCGGAAACGAGAACGTGTTCCATTATTAGGGTGTGAGCACCAATACCAGATTGCTCACCA
CTCACCGCAGCACCAGGACGGATGTGGCCACCACGCCATCTGGGTGGTAGCGGGAAATACCGCTAACGGCTCC
GGTGGCG (SEQ ID NO. 586)

Clone Rv48

:::::::::::Rv48SP6.seq:::::::::::
TACTCAAGCTGTCAAATATCGAACGCTCGGTCGCGAGGGCTCGTCGGCAGCTCCAGCAAAACCCGCTCCACCC
AGATGCCGGTATCCCTCAAGGTCTTATCCGCCCTCACCCACTGGCACACGGTACCGGACGCCGTCGCCCCCGGCC
ATGGCGCGAACCGCTGAAGCGGACCCGACAGCCGCTGCCGTGATGGACTGATCGCGATCCACCCGGCATGGCCGG
GCTATCCGCGGGAAAGTTGCCGGTCCCCGCCACATACAGCGGAGGATAGGGCTTGTGACCGGCTTCGGCCAGCAG
TAGATCGGATCGAACATATGCCCCATGGAATTCCGCCCTGCTCTGCGTTAGATCTGATTATCGCGCAGAAC
CGCTCATCGATCACACGTCCCGCACCGCAGGGTCCACACCATGGTGGGACTTCTCGCGCAACCAGCCACACCA
CGCCGAAACGAAACGTCCCTGCG (SEQ ID NO. 587)

:::::::::::Rv48T7.seq:::::::::::

CAGGCATGCAAGCTTGGCAACTCCTCATCGGACTTGAAGGTGCCGTCCTCGTTGGCGGCCCTGCTCACGGCACGTT
GATGGCACCAAGGAATGTGTCGGGGCGCTGGCTTGTTCCTGCCGAGGTGCGCGGGGGCCAGGATCTGCCGGAGAA
CTCGTGGGGAGAGCGCACGTCGATGAGGTTCTGACGTTGATGCCGCCAGGACCTCGTCCGGAAATGCCGAATCGT
GTATCCGGGGGGGANGCGGTGAGGAAGTCACCGGCCGCTGACCGGGTCGCTGGACAGCGGGCTCCGAGCTC
C (SEQ ID NO. 588)

Clone Rv49

:::::::::::Rv49SP6.seq:::::::::::
ATACTCAAGCTCAAAACAGGCCTGTTGTGGCGCACCCGCTGCCGAGTTCTGCACGCACCGCCTCAAGTGC
CGCACCGCCGGCATCTCCGGTCACGCAGGGCCGCCGCGCAGCGACGGCGTGTTCGCGCAGTTCGCGTCA
ATGATGCTGACCTGATCGGCCACCCGGCGGTCTCGCGTCGTTCACTAAATCGCGGTCGCTCAGCAGCGTCTCG
ACAGCCACCAACCGAGTGGAGACCAAGATGCNCCACCGACCGCAGCGATGCCACCTCACCGTCC
(SEQ ID NO. 589)

:::::::::::Rv49T7.seq:::::::::::

CAGGCATGCAAGCTTGCAGTTGCTGAGTAATGTCGGCAACGTCACCCACAATCGCGATGAATTCAATCATGCC
AGGGCGGCCAACCAATGGTGGCCGAGCGGGCAGCTCGATCGCAGCGCGAGGGTTGCCGGCCAGTGTGATTCA
AACAGGGTGAGGTATAGGCGGGCAGGATAGTGACGAAGGCAAGACCTAGATCTGCCGTCGGAAGAAGAATCGAGT
CCGGTCGACACAACGGAAGCGAAAGTGTCCCGATGTTGAGCGTCGCCGGTGTGGCGGGTGGCGGGTAC
ACCGTCCGACATACCGCGGGAACCGCGGGCATCCGAATTGGGGCAGGGTGTCAAGGCGGCTGGCAACTCACC
ATGA
ATCT (SEQ ID NO. 590)

600
 ATATCTTAAGCGTCGGTCCCGAGGCTCGTCGGCAGCTCCAGCAAAACCCGCTCCACCCCTAGATGCCGGTATCCCT
 CAAGGTCTTAGCCGCCGTTACCCACTGGCACACGGTACCGGCACGTCGCCCGGCCATGGCGCGAACCGCT
 GAAGCGGACCCGACAGCGCTGCGGTGATGGACTGATCGCATCCACCGGCATTGAGCCGGCTATCCGCGGGAACT
 TCGCCGGTCCCCCGCCACATACAGCGGAGGATAGGGTTGTCACCGCAGCAGTACGAGTGGATCGAAGT
 CCACATATGTCCCAGGGATTCCGCTGCTCTGCGTCCAGATCTGATTATCGCGCAACCGCTCATCGATCACAC
 GTCCGCGCACCAGGGTCCACACCATGGTGGCAGTCTCGCGCA (SEQ ID NO. 600)

Clone Rv54

:::::::Rv54SP6.seq:::::::
 ATACTCAAGCTTGTGCGGGTAAACCCGAGCAGGGCGGTGGGTGCGGTGCAAAAACAACCACACTTCTTGCGGTT
 GGTGATCTCGACACCAGGGCGAGCCGACCCATGCGCGTAAATCGCGATCAGCGCTGGCTATGCCCTGGGT
 GCCGCCACCGGAATCGGCAGCCGACCGAATGGGCCAGCGTTGCCAGCATCAGTCCGGGCCGGCGACACCACTGA
 CGGCAACGGTGAATCGGTGGCGCAACGCCGTGAACAACGCGCAGGCGATCTCGCCCGCAGCGACCCGCAAGG
 AGGGGTGCCCTGGGCCAGCATCCGAGCCGAGACGAGGCCAGTGCAGTAGGCAAAGACCGCTGTCGGA
 GACATGAACCTCACGACCGT (SEQ ID NO. 601)

:::::::Rv54T7.seq:::::::

AGCTTATTGAAACCGCGGGTGCAGGAAAGTGGACCTCATAACGACTCGGGTCCAGCGACCGGCCAACACGAACGGC
 CGGACGACGTGGGCCAGGGTGCAGGGCTCCCTACAAACAGGATCGCTGCGAGCGACAGGCTCCGGTGCAGGG
 TTGGCGCCGTGCTCGTCCAGCGTCCGGTCCGGTGCAGCGTGTGTTCTCCATACTCGCCCCCTAATCT
 CGAGGCAGCCCGTACCCGAGGCAACCTCCAAAAATGCAATCCCCAAAATGCAATGCGTCAGCTATTCTCACAC
 CGACCGCTAGTTGCGGATCAGAAATCGTTGGCGGAAAGTCCAGCGAATTGTTCTCCGCTCCGATCATGCTT
 GTAATCGTTGAAATTCATCCTCATATGCCTCGATCGCTCATAGGGTCCAGGCCAAACCGGGCA
 (SEQ ID NO. 602)

Clone Rv55

:::::::Rv55SP6.seq:::::::
 CTTCCGGCTCGTATGTTGTGGAATTGTGAGCGGATAACAATTACACAGGAAACAGCTATGACCATGATTACGCC
 AAGCTATTTAGGTGACACTATAGAAACTCAAGCTTGGCACCTCGGGTGTGTGGAAACCCATCTGAGCAGTGTG
 CCAAACGGGGCAGACAGCTCCAATTGACGTGAGCCGCTCACTTGCTGGTAAGCGTCG (SEQ ID NO. 603)

:::::::Rv55T7.seq:::::::

TAGCGCCCCCTCCCGGGCGGAGCTCCACGGCGTGGATCAAGGTACCGCCGGATGTTGCGCAATGGCAGGGTTG
 CCGGCTTGTGTCGGCTTAGCGCCGATTCCACACATCCCTGCAAAGTCCGGTGGTCAATGATGTCAGCGCT
 TCTCCCCATCGAGATAGTGGAGCAACGCAATCGTGCCTGCGTACGGTTGGGCGTACTCGATGTGCGGACCTTGGCGT
 TGACACCATTGTCATTGCGGAAAGTCGATCATCCGTAAGCGCTTATGACCGCCGCTTGTGCGGGTTGACCGGGTGA
 TAATCCGGCATGCGCTTGCCTCACCGCGACCGTGCAGCGGGCGCACAGCGACTTCTCGGGGTTGACCGGGTGA
 TCTCGGCAGGATCAGATACGCTGGCGCGACGACCAAGCGTGTGGTTGCGAATTGCAATGCTAATCA
 GGTCTTCTC (SEQ ID NO. 604)

Clone Rv56

:::::::Rv56SP6.seq:::::::
 TGAAACTATATAACTCAAGCTTGCAGGAAAGAGACCTCGTCGACCAAGCAGGACGCACCGTCGAGGTGGCGATCCG
 GCTTGGCGTCGACCCGCGTAAGGCAAACCCAGATGGTCTCGGGCACGGTCAACCTGCCACACGGCACTGGTAAGACTGC
 CGCGTGCCTGATTCCGGTTGGTGAAGGCGATGCTGCCGTTGCCGGGGCGGATGTTGTCGGAGTGCAGA
 TCTGATCGAAAGGATTCCAGGGCGGGTGGCTGGAATTGATGCCGATCGGACACCCGATCAGATGGCAAAGTCGG
 TCGCATCGCTCGGGTGTGGTCCCGCGGGCTGATGCCAACCCGAAAACCGGACCGTCAACCGCCACGTCGCAA
 GGCGTGCCTGCGGACATCAAGGGCGGCAAGATCAACTTCCGGTTGACAAGCAGGCCAACCTGCACTTCTC
 (SEQ ID NO. 605)

:::::::Rv56T7.seq:::::::

GCTGAGCTCCACGGCGTGGATCAAGGTACCGCCGGATGTTGCGCAATGGCAGGGTTGTTGCCGGCTTGTGTCGGC
 GTTAGCGCCGGATTCCACACATCCCTGCAAAGTCCGGTGGGCGTCAATGATGTCAGCGCTTCTCCCCATCGAGATA
 GTGGAGCAACGCAATCCGTGCCTGCGTACGGTTGGGCGTACTCGATGTGCGGACCTTGGCGTTGACACCATTTGTC
 ATTGCGGCAAAGTCGATCATCCGTAAGCGCTTATGACCGCCGCTTGTGCGGGGTTGTAATCCGGCCATGCGC
 GTTGCCTCCACCGCGACCGTGCAGCGGGCGACCGCAGCGACTTCTCGGGGTTGACCGGGGTTGATCTCGGGCAAATCAGA
 TACGCTGGCGCCGCGACGACCAAGCGTGTGGCTGTACTTGCGAATTGCCATGTCTAATCAGGTCTTCTC
 (SEQ ID NO. 606)

Clone Rv57

:::::::Rv57SP6.seq:::::::
 ATACTCAAGCTTGTGGTGAACCTCGCCGGCGAACAGTTCTGCACGATTCCGGATTAGCGGGACTGGTCACCAGTTG
 GGTATGCGGAAAGGCCTGACGTTCGCCCGATTAGCTGTTGATGGACCGCGGTTGATGTCCTGATCACGGAACCTG
 GCTGTAATAGCCAGGGTCGCCACGCTCCATCCGGGCCGGACCCGGC (SEQ ID NO. 607)

:::::::Rv57T7.seq:::::::
 GATGATGCCGGTGCCACCCGATCCGTGCCTCGGTCAGCGCGAACAGTGTGTTCCGGTCCGGCGACCACCATGTCGA
 CGCACCGACCAGGCCAACCGCCGGCCGACATGCCGTTGATGGCGCCGACCACCGGAGCGGGGACTCGACGAT
 GGCGCGAACAGCGCCGTCAATTCCCGGCCGGCCACCGCCATCCGGTACGGATCACCACCACTCCGCCGGCTC
 GCTGAGGTCC (SEQ ID NO. 608)

Clone Rv58

:::::::Rv58SP6.seq:::::::
 ATACTCAAGCTTGCCTGAATCGAAACCAACCTGTTGTGGCGCAAGAAATTACGCCGTGGCCCGCGCATAAGAA
 ACGCCCCGGCGCGCGGGTGTGTCGTATGGCATGACGGGACCAATGTGACGCCATTGTCGAGCAGGCACCGGTG
 CCAGCCCCCGAACCGGGTGCACCAGGGACACCCGGCCACACCCGGTATCGACGGCGCTGCTGTTGCGCTGTC
 GCCAGCTCGCAGGACCGCCTGCGGAAACCGCCGCGCTGGCGATTGGTCT (SEQ ID NO. 609)

:::::::Rv58T7.seq:::::::
 TTGGCGGGTTGGCCACANCANCCGCCGGTGA CGCGACGATGCTGGGCTGGTTGCGGCCCTGCGCCACCGCGGCTTG
 CATGCTGGTTGGCTGTCTGGGACGATCCGAAATAGTCCACCGGGATCTGGTATTGCGGGCTACCCGCGATTAC
 CCCGCGGGCTCGACGAGTTTGGCTGGACTACCCGCGTGGCCAATCTGCTGAACCTCGCGGCCGGTGGTGGCCTGG
 AATGTCANCGCCGTTACCTACGTGACCTTGATGGGATCCGGGGNT (SEQ ID NO. 610)

Clone Rv59

:::::::Rv59SP6.seq:::::::
 NCGTGGACACCGGTGTCGANCGCCACAGCCGATGTCGANCAGTCNATTCCGTCCTCGGAAACATCTGAATGCCGA
 GCAGCGCCTGGCGTATCGGCAACCGGGGATGACCGCTCGGCGATCCGCTCGACAATCCGGCGGACGTGACATGC
 CGGGGACGGCTCGACGAGCTGGAACTTCAGCAGCAGATCCGAAATTGATCACCACGGTGTACTCATGGACC
 CCTGCGCCTGAATCCGTATGGCACGGTGTGACTATTGTCGACAGTGCACCCGAGATAGTCTCACGGCTGCGT
 (SEQ ID NO. 611)

:::::::Rv59T7.seq:::::::
 CATGTATTGCCGTGTCACGGGCCACGCTCGATGGTTCTCGAAGTCTCGGGCTGGTGTACAGCTTCTCGTTGATC
 TCGCTGCCACGCCGTCCTCTCCGCCGACGACCGATCTCGATCTCCANAATGATCTTGGCGCCGCCGCCCT
 GAGCAGCTCTGGCGATGGCCAGGTTCTCATCGATGGGACTGCCGACCGTCCACATGTGCGACGGAACAAAGATG
 TCACCTGCTCACCGTGCNAGATNCANAAGGGCCGGACATACTGTCNACTTGTCTTGGCAGTGGTCCGTGTC
 AGCCCACGTGACGGGTACTTGGCGCATAACGTGGT (SEQ ID NO. 612)

Clone Rv5

:::::::Rv5SP6.seq:::::::
 GCCACACGACCCGGCGTAACCTCTGTCACGGAAATGCGGCCAGGCCGCGTAGCACGTGGTATCCGCCATAAAGG
 TGCACCTTAAGCACGGCGTCCCAATTCTGAAACGACATCTTGATGGAAAGGTGCGCTCGCGCAAGATCCGGCGTTGCTC
 ACCACACCGTGCACGGCGCGAATTGTCAGCGCGGTCTTGATGATGTCGCTGCCGCGTCCCTCGGTGGCGACGCTG
 TCCTTAGTTGGCGACCGCCGGCCCGTGTGCGGAATCTCGCGACGACCTCATCGGCCATCGCCGAACGGCGCC
 GTGCCGTCGGCGGCCACCGAGGTCGTTGACACGA (SEQ ID NO. 613)

:::::::Rv5T7.seq:::::::
 CAGGCATGCAACCTTGTCCACACGGCGTCACTCCGTGCAAGGTCCGACCGCTTCCACGTCCGCCGTGACGGTGCT
 CCATCTCCCTCAGCAACCGGTGAAGTGGTCCGATCCCGCGGCTTCAGG (SEQ ID NO. 614)

Clone Rv60

:::::::Rv60SP6.seq:::::::
 GTTGAGACGCAACCGCGCACAAACGACGATTGGCGTAGCGCCGGACGTCTGCTGATTCGATCACGTCGCGCTCGCA
 TCGAGCATGGCCCGCGACGCTACACGATCGCCGTCGATGACAGCAGCCGACGGCTACGCCGCGTAAGCCGCGCC
 AGGATTGGCGAAAAACGCTACGTGGCGGGTGTACTGGGTGCGAATGATCGTGGGTTGCGTATGCGTCTGCAAT
 CGTCGACATAGATCCGTGCCGCATCGCGTCGACAACCTCCGGTGAGTGGAAACACTTGCCGATCACGCGACGTGCG

CGGATCGATGCCGACCGAAATACGACCACATGGCTTGTGCNCAGTGTGGCGGCATCAAATACCTCAGTGCCTG
 CCGAC (SEQ ID NO. 615)

:::::::Rv60T7.seq:::::::
 TTNCGCCTTACGCCTACTCCNAGACGATGCTGACCGCTGTGAGCACACGGCGCTGCTTAGACGGCACGGCGCAG
 CTGGATCGCGCTTGGTGCACCCAAAGCCTCTACCGCGCTCGCTCGTCACTCGGGTACCGAACATATTCCGGTCGTT
 GCGCAGAGTGTGATGTGGGCTTTGTGAACGAAACATAGCAAAGCTATATGTCGTGGCGCTCTGCAGATATCGC
 GATAATACGTATATACTAAGTGGCGCGATCTATCGGTATATCGTTATGGCGGACGTGCCTGAGCGTGAGTCGC
 GGCGCATCGCGACTTCGCGATCGCGTGAUTGGTCTCGCGACTGCCTGCATCGCTAGC (SEQ ID NO. 616)

Clone Rv61

:::::::Rv61SP6.seq:::::::
 GGTGATGACGCACTTGTCTCGAATGAGTCATTGACTACTCCGTGGTTGTCCCTGCATGGTGGAGTGCCTGCAGCCT
 TGCCCGANGTCGCGATCGCGTCCGGCTTCGGGGAGCAGACTGACCTGCAGATGAAAGTCGTGCCACATGCCCGCGA
 ACGGCGAGCTCGATGCTTGTGAAGNGCGCANGCGGTTCGATCTTGTCCCGTCAACGCAGATCGGATCTCGCC
 GCGGTCTGCATGACGATGGCGCAGGGCCGCTATGTCCTCGTAGACGGGGAGATACGGGAGCCGCGGATCGAGACCT
 ACGTAGCGCGGCCCATCGCCATCGACGAAGAATGACGGATCGCGAGCGCCGTGCGTCGCTCGATGTCACGC
 GAGATGCCACGGCAGATCGGATGCCAG (SEQ ID NO. 617)

:::::::Rv61T7.seq:::::::
 CGGTACGCCGCAACAAACGCCCTTGTGACGAGCGCTCCAGCGGTCACTGGCCTCCACCGTCATGCACAGCTCCTTC
 TCCAGGTCTACGCCGACGTGCGGGTCCACATTGGTGAAGCTTGGCGAATGCCCTCGTCAACATGCCCTCC
 GCGTCCGCATCGAAGGTGCCATGTCAAAGATCAACTCGACGTAGTAGCTAGTTACCGCATCAGGTAGTGTGCGT
 GCCTCGGAGTCCGGCGAACAAATGCCATTCCCGGACTCTAGAATCCAGTCATCGTCTCGGTGACGACGCCCTGCG
 GATCACATAGCTGACCGGATCGGAGAGAATCTGGTTCTCGT (SEQ ID NO. 618)

Clone Rv62

:::::::Rv62SP6.seq:::::::
 ATACTCAAGCTTAAGCGCAGTACCGCGGTGCCTGGCATCCAGAAAACGGGAGCTCACGAACGATTCTG
 AACGAAGGGTGTCCACCAACCTCCAAACCGAACGGTTGCCAGCCCCGGC (SEQ ID NO. 619)

:::::::Rv62T7.seq:::::::
 GCAAGTCCGCTCAATGTGGTTGTGATCACANGACTACGTGCCCTCAATCAGCTCAAACGTCAACCCGTGGCGTGC
 GCAGCATGAAGGTGGCGCCCGCACGATGTGGCGAAGCAACAGGTAAATACTGGTCCGGCATGGTCAACCCCTATTG
 GGCGTTGCGGATCGGGTGCACGCCCCGAGTGCCTCGAACACTCACCGCCTCACCGATCTTGTGCGAAAATG
 GCGTCGTGTCGGGTATACGTCCGCGATCCACGAGGCGGAATCCGCTGAGCGCACTGA (SEQ ID NO. 620)

Clone Rv63

:::::::Rv63SP6.seq:::::::
 ATACTCAAGCTCGCCCTCAAGCGGCTGAAGGTGGTCCGGGTNCACNGTCGGGAACTCGCCGATGGCATG
 GTGCTCGACNCCGCTCCGGTATCCCGGGAGCTGCGCCCGATGGTGCAGCTGCAGGGCGGTTGCCNCGTCC
 GACTTGAACGACCTGTACCGCAGGGTATCAACCGCNACNNNGNTGAAAAGGCTGATCGATCTGGTGC
 ATCGACAATGCCGCCGCCGGCCCGGAAATCATCGTCAACACNAGAANCGGATGCTCGNGGAATCCG
 TGGGACGCGCTGTCGACAATGCCGCCGCCGGCC (SEQ ID NO. 621)

:::::::Rv63T7.seq:::::::
 TGGCATGGCAGTTGTGCGGGCTTGTGAGTCGCTTAGCGGGATTCCACACATCCCTGCGAAGTCGTGGGTGCAAT
 GATGTAGCGCTTCTCCCATCGAGATAGTGGAGCAACCAATCCGCGTACGTTGGTGTACTCGAGTGC
 GCGTGTGACACCATCTTGTGATCGCGCAGGTCGATCATCCGTAAGCGCGCTATCGACGCCCTGTGCC
 GTGGTAATCCGGCATCGCGCTTGCCTGCCACCGCAGTCAGCGGGCGCACACCGACTTCTCGGGTACGGGTGATC
 TCGCGAATCAGAACCTGGCGCGACACAGCGCTGTGGCTACTTGC (SEQ ID NO. 622)

Clone Rv64

:::::::Rv64SP6.seq:::::::
 TGGGTGATCAGATACTGGCTAGTTGGTGGGTGATCGAAGATCGCGGTGGCGGAGCGTTACTCGGGTGACG
 CTGTTAACCGGTTACGTACTCCACGGCACTCAANGAATTANATCCGAATCGGAAACCCCTGGCCAGCGTC
 GAGCGCCGTGCGCCCCCACCCTGCGGATGCTCACATACCACCTCGATCGTGCAGGGAGTTGCTCGT
 CGACCGGGCGCACACCGACTTCTCGGGTACGGGTGATCGC (SEQ ID NO. 623)

:::::::Rv64T7.seq:::::::

TCGTAGCGGTTGCGACCANTCCGCGGACAGCTCCGCCACGCCACGGGTCGGGATCACCGCGGTCAAACCACCGAGCGG
 CGAGGATCTCTGGCGTCGACGTGACCGCGCACGCCCGGGTATGGCCAGTCCCGACCGCCGTTCACCTGGCGTAC
 GCGCTGGATGTGTTGCGCAACGGAATCCCACCTCAATTATGACCTCGTTGTGGCGAGCGCGGTATCGTACGCC
 GACCAGGAATCGTCGATGCTATCTCACGTACCGAAGGCCCTCTCCAGCACCCGATCCAGAACGTGACACNGTC
 ACATGTCTCGCGGATCCGCGTGCAGAACGAAACGCCANGTGGCTGTGCGACACGGGTCGGATCACCGCTCGCACGC
 GGAGATCGGCACACGCGCAGCGCATCGATCATAATCTCTCGATGCGGTCTCCACCAACCGAACAG

(SEQ ID NO. 624)

Clone Rv65

:::::::Rv65SP6.seq:::::::

ATACTCAAGCTCGCTGAGGTGGTGGGGCACGATCACGTACCGCACCCTGTCGGTGGCGCTGGATGCCGGCCGGAT
 CAACACCGCGTACCTGTTCTCTGGCGCGTGGCTGCGGAAAGACGTCGTCAGCGGTATCCTGGCNCGGTCGTTGAA
 CTGTCGGCAGGGCCCTACCCCAACCCGTGCGGGGCTGCGAATCCTGCGTTCTGTTGGCGCCCAACGCCCGGAG
 CATCGACGTGGTAGAGCTGGATGCCGCCAGCCACGGCGGCTGGACGACACCCGAGCTGCGGACCGCGCGTCTA
 TGCGCCGGTCCACTCACGGTACCGGGTATTATCGTCGACGAGGCGCACATGGT (SEQ ID NO. 625)

:::::::Rv65T7.seq:::::::

GCACTCACGCTGGTACAAGACCTTCACAAAATCTGAAATCCTGACCCGATACCTGAAACCTGGTCTCGTTGGCAATAA
 CTCGTTCGCGTGCAGGACCGCGCAAACGTAACCTCGGCATCAACCGTCCGACCTGAATTGGCAGCAAGCGCGCT
 GCTGGCCGGATGGTGAATCGACCGACGCTCACCCGTACACCAACCCGACGGCGCGCTGGCCGGGAGCGT
 GGTCCTCGACACCATGATCGAGAACCTTCCCGGGGAGGCGGAGGCGTTGCGTGCCGCCAAGGCCGATCCGCTGGGGGT
 ACTGCCGAGCCAATGAGTTGCCCGCGCTGCATCGGGCCGGCGACCG (SEQ ID NO. 626)

Clone Rv66

:::::::Rv66SP6.seq:::::::

ATACTCAAGCTGTATAAAAAGATCGGTGAGCGCATCGATTGCTCCGCCGGGTTTGCCGCTGCCGCCGGAGCTGC
 CGTACCGTCTATTGGGTGATCAGATACTGGGCTAGTTCGTCGGGGTGGGGTATCGAAGATCGCGGTGCCGGCA
 GCGTTACTGCGGTGACGGCTGTTAAGCGGTTACGTACCTCACGGACTCAAGGAATTAAATCCGAAATGCCAAACG
 CCTGGCCAGCGTCAATCCGGCAGCGCCGTCGCGCCCCAGCACCGTGCAGCTACATACCCATCGCTG
 CGCGAATTGCTCGTCGGCGACCGACCGGGCCAGCCGGGCAAACCCGGAAGA (SEQ ID NO. 627)

:::::::Rv66T7.seq:::::::

CCTCATCATATGCCGATAGAGCTCTACATATTCAAGGAGATCACCATGGCTCGTCGGTGGGATCGACTCGGACCAC
 CAACTCCGTCGTCGGTTCTGGAANGTGGCACCNGTCGTCGTCGCCAACTCCGAGGGCTCCAGGACCACCGTC
 AATTGTCGCGTTCGCCCCGAAACGGTGAGGTGCTGGTCNGCCAGCCGCAAGAACAGGAGCTGACCAACGTGATCG
 ACCGTGCGCTCGGTCAAGCGACCATGGGAGCGACTGGTCCATAGAGATTGACGCAAGAAATACGCCGGAGATCT
 CGCCGATTCTGATGAACTGAACCGACCCGAGGCTACTCGTGANGACATNACGACCGTTATCACACCCCGCCTNC
 TTCAATGACCCACGTCNGGCACCAAGGACCCGCAATCGGGCTCACTTNGCGATNGTCNACAACCAACCGCGNC
 CTGGCTACGGGCTAACAGGACACAAATCCGCTCGATTGGTG (SEQ ID NO. 628)

Clone Rv67

:::::::Rv67SP6.seq:::::::

ATACTCAAGCTTATCGAGCGGGCGCATACCGAACGCGTGGGAAATCCAGACCGAATACCGCAGCTGCTGGACACTTGG
 GCGCGAGCTGCTGGAAAAGGAGACCCCTGACCGACCCGAGCTGGAAAGCATCTCGCTGACGTCGAAAGCGGCCG
 CGGCTACCATGTTGACACTCGGTGGCGGATCCCGTCCGACAAACCGCCCATCAAGACACCCGGAGCTCGCG
 ATCGAACGCGGAACCTGGCCCCAGCCGGTCCCGAGCCGGCTTCAAGGCGGAGTGCATGCTACCCAAAGCC
 GCTGAGGCCGGCCGGTCCGACCCGGCAAACCGGGCACGGGCCAACGGTTCGCCCCGGCACCACCGGTCGGTGA
 CGCAGTACGGTCCCCCGCCTGACTACCGTGCCCGGGCG (SEQ ID NO. 629)

:::::::Rv67T7.seq:::::::

TGGCGGGCTGGTAGCCCCGCTATGCGAACGGTCCGCTCAATGTGGTTGTGATCGACGGACTACGTTGCCCTCAAT
 CAGCTAAACGTCACCCCGTGGCGTGCAGCGACGATGAAGGTCGGCGCCGACGATGTGGCGAAGGAAACAGGT
 AAGAACCTGGTGGCATGGTGCAGGCCCTCATGGCCGTTGCGGATCGGGTTGCAGCGGCCGGAGTGCCTGGTCA
 CTCAACACCGCCTTCACCGATCTTCTGTCGAAATGGCGTGTGCTCCGGGTATACGTCGCGATTCCACGAGGCG
 GAATCCGCTGAGCGCAGCTGATCCGGCTCGCCGCGCGTGAACCTGGCTGTGGTTGAGCATAACGAGCAG
 ATGCGAAT (SEQ ID NO. 630)

Clone Rv68

:::::::Rv68SP6.seq:::::::

GTCCAGTCAAGCATCGGTCTCTCGACTACGCCAAGANTGGCGACGTGTCAGTGCANACAGCGGANATGGTGGCGCC
TATGCGTCGACGCTCACAAACNGCGGTGANC CGGTTCTGGTCGTGACCATCGAGCCGTGCCAGCCCGGCCGCGTGCC
GTCAGCCGCATCCACTGGATGCCCTCTCGGNGTTCAATCANGTACANGCGACGTTGCCACCATCGTGCCGGGGCAC
GGTTAGCGAGAAACCGCCGACTTCACCGATTGCCCTCGGTGATGCCGTGAAAGATCAGGGCTATTGTGACAGCCAG
TGTGATNCGTATTTGCCGCCGTGCTCCTCGTCGCAACGATGCCAACAGATCCGTGGNGGACGATAGCGGCTGACAA
NGTGGGGGCAACACAATCACATGCCACATTCTTCATTCACGCCACAAACCCAGACTCGTCTCGATGNGCCG

(SEQ IDNO. 631)

.....RV6817.seq.....
CAGCCGGTCTGGCCCCATCCGAAGATCCCTTTGCCG

CACTGGGTCTGGGCCGATCGAAGATCCCTTGTGGCGCTGGGGCTCTGTCGGGGTGTGTAACACTCTCGAACCA
CCTCGGACCCGACACCACCGACCTNGCTTGAACACCAGCCAAACATCGGCAGCAGATCTTGATGGTCTGGTGAATCCCC
CGGTGACTTGGAGTGGAAAGGCCCATCTGATCGCCGCCAGCACATGAGCTAGCGCAGGAAACCCAGCAGCCGC
TCACCTTGCAGCAGCGTCGGTGATATGCTGGCCCTTAATCTGTGAACCAGTGGATTGGGTCAACTGGCAG
CCTTGGGTCTCGGTGGTGCCGANGTGTANATAAGCTCCCGGGTCCGTCAACGTANTGCGCAGGCGGCGTTACTCGG
CGGGTCAACGAGCCCGCTCGTGAGCNATCAGCCTTGGACCGAACGGGATTCATACTCCGCAGGGGCCCTCCGAAA
TCGGCACATGTCTTGATCGTCGAACAN (SEQ ID NO. 632)

Clone Rv69

|||||||||:By69T7D3.seq|||||||||

GGCCATGTCACATCGGTGGTACAGGTAACCGCGCCGTGCGCGGCTCGGAGATCAGAACGTGGTCGAGTTGACCGCGGGCTTTCAGCAGTCGCGATAATCGCGGAAGTCGGCGCTGCCGCCCAACTAGCGCAGTCGCCACCTAGCACACCGATGGCGAAGGCCATGNTCCGGCACGCCGCCGCGGTGCATCACCAAGTCATCGACTAGGAAGCTAACCGACANCTTGTGCAGGTGTCGGGCAGTAGCTGTCGGAAAATCGGCTGGAAACCGCATCAAATGGTCGGTCCAATCGAACCGGTTACCCGATCGTCACAAAAATCTCCGTCT (Seq ID No. 33)

Sloan Doc

clone RV6

.....:RV6SP6.seq:.....
GGGTCTACAACCCACGGGCTGACTTCTGGGCTTCCACCGCTCGGCCGTCGCACAAACAGCGGGTCGAACCGACAGCTCGTTGTGATGTCCAGCTATCACCTCCGGTAGGCACCCAAATCGACCCCTACCCGGCTATCTCACCCCCGATCTCCAGGCTCCGGCGATCCATGCGCATCCCGGTCGGATCCC (Seq ID No. (-3u))

(SEQ ID NO. 635)

Clone Bv70

BY70SP6D2.seq

.....RV705F6D2.seq.....
NCTACGCTGCTGAATGTTGTGGCCGGAGGANCTCAAGACCCACGCGGTTGTACGCGGACNTGCGACATGTTCAACCG
CCGGA (SEQ ID NO. 636)

Rv70T7D3.seq

CTAACCAACAAGCCATGGTGGTGGCGCCGTCGAGAGGTCGGCGGTGCCACAACGGGAAGATGCCCTTGAGCGTCGC
TCGACGCCGCGCTCGAGTGGGTATAACGAAGTACTGATGCCGATCATGTCGACGTGTCGTCGATCAGCGTGCAG
CGGCGACCCCTCGACGAGCCTGGTGCCTGGCGGCCAGGGCACCAGCTGTTTAGCGCATTGTCGTCGCCGGTAAT
AAAGGANGTCGGTCGCCCTCCGCTGCTGGTTGCGGAATAACATCTTCCCTGCAACAGGATGAGAATGGTTTA
ATTGCTC (SFR ID 10637)

2000-02-01

Clone Rv71

:::::::::::Rv71SP6.seq:::::::::::
CTAACGCTTCCGGTCCGCCACTAGTACCGCGTGCCTGGCCCGGCCGACCTAGAATGTTCCGCCATTGCCGTTCC
CTCCCGCCGCCGGGTT (SEQ ID NO. 638)

:::::::Rv71T7.seq:::::::
 TCTGGTGCCTGGTGTGCCGACGGGTCGTCGCCCTCTGCTTCAGT GATTCTGTGATGCGACCGGAAACGTCTCGTTG
 TTCGGTGTCTATGTGGTCCGTCTCCTTGTCCGCATACGATT (SEQ ID NO. 639)

Clone Rv72

:::::::Rv72SP6D2.seq:::::::
 GCGATCGNTACCACAAGGGCGAACCGGTTGCCGCGTCGACTGAACGTGCTGCCGCCTGGAGAACTGGCGCTGCTGCC
 ACCTGGTCGGCGCATCGGCACTTCGAGGACTGGATTTCGACCGTGGCCCGACCTGANGTNGCGGTGGACNNGTGTG
 CACCCGGTTGATTCTCGGCCCTGCCGGGATGCCACCTGCCGCTGGTGGTCGAT (SEQ ID NO. 640)

:::::::Rv72T7D3.seq:::::::
 CGT GACCGGACGGGTGCCCGCGAACCGGTTGCCCAATTGCCGGGACTGGGGCTGGAGTATAAAGCAGGGCCTGT
 TGCCGGAAGATAAAGTCAAAGCGGTGACCGAGCTGAATCAACATGCCGCGCTGGCGATGGTCGGTACGGTATTAACG
 ACCGCCAGCGATGAAAGCTGCCCATCGGGATTGCAATGGTAGCGGCACAGACTGGCGCTGGAAACGCCGACGCA
 CATTAAACCATAACCACCTGCCGGCTGGTGCACCGTGGCACGNCCACTACGCCAATATCCGCCAGAAC
 TCACTATTGCCGCTGGG (SEQ ID NO. 641)

Clone Rv73

:::::::Rv73SP6.seq:::::::
 ATACTCAAGCTCTTACCCANAGCATGAAACCCCGCCGTCCAATGCCGCCACCGTGGTGTGTCGGCCGGCCGGTGC
 GGCACAATCGCCGAGTTCGGCGAACAGATCCTCGAAGGTCTCACGGCAGCGATTGTTGCACGTGTCAGCCAGCCAA
 GTCACGGTGGTTGACGCCACAGCTCGCCACCGCCGCCGCGCATTAGGGCATCCTAATATAAGGTTAGGCTACCC
 ANTATTCTCTGTGGTCNAAGGAGGCAGCCGAAACGTGACCTTCCCGATGTGGTTCGCAGTTCCGCCGGAAGTGC
 GCATGGCTGTCCACCGGCATGGGCCCCGGTCCGCTGCTGCCGCCAGGGCGTGGCACGCCGCTGGCCGCCAATAC
 ACCGAAATGCAACCGGAACTCGCAAGCGTGTGCTCGCTGCCGTGCAAGGCAACTCGTGGCAGGGGCCAGGCCGACGG
 CGTCNTCCCCATCAACCGTCCGTATTGGCTAACCGTGCACGGTGGCACCGCACAACGCCGCCACAAACGCC
 GGTATAC (SEQ ID NO. 642)

:::::::Rv73T7.seq:::::::
 GGCGAACCTAATCGGTTGTTGGCGGCTGCCGAGTTGGTCACTCGGGGGTGTGCACTGGCACATGGTGGCCGGAT
 TCAACGCAACAAAGCGGGTCGCTGGCTCGTGGCGAACACCGCTCACTCGTGGCACAGCTCGCGGTTGGACCGC
 GCTGGATCGGGCGGTTGTTGCGGCCTGGCGAACACCGCTCGTGGCGAGCGGCTGGGGTTACGTCCAGGTCA
 CGACGGTACGGATCCCGGGCGGCCGTCGACAGCACGACGCCGGCGCGTAGACCGGATTTCGCGCGCAGGTGCA
 GTCAGAGGGCTCGAACCTGGTGGGTGATGGGATTCCGCCCTGGATTGGGACCCGACGAAGCCTTGACCGGCTG
 CAATCGGAGCACACCGGGTGCCTGCGATGTTCCCGCACGCCATCGGTCTGTCGCCGATGTCCAACAACTGAA
 CCCGTCACATGGTCGAC (SEQ ID NO. 643)

Clone Rv74

:::::::Rv74SP6.seq:::::::
 GCTTCCCTGATACTCGACCAGCCCCACTCGGGCCAATACGTGAAATGCTCTAGCATTTTACCCGTTACGGGCTAG
 TCGAGTAGACGATTGATTAGCCTGAACGTACCTCGACGGCCAGCTGACGAACGGTTGACGGA
 (SEQ ID NO. 644)

:::::::Rv74T7D3.seq:::::::
 TCAGCTGTCTGAGAAGGGCTGGCGATACTGTGCACTGTCTGATATCGCNCNTGTTGGGACTATNCAGNCATNANG
 ATGCCGTTCNNGNNNTGCAGAGNATCCTGGNACACATCGGTTACGTTAATCANCATCGCAGNTNCTNCGTNTTCG
 ATTANTTCTGCTAACGNNTCTNNNAGTGCCTGCCGTGACTCTAGAG (SEQ ID NO. 645)

Clone Rv75

:::::::Rv75SP6D2.seq:::::::
 NCTCTGCCGGGCNAGAGCGCAGAGTCGGACGGCTCGTCGATCGTGAAGCGACCNNTGCGATGANCAGATATCGNTNAC
 ACTGCTCANAAACTTCGGATCATCGNTGATACACAGGCCAACGGGTAGCGGTTGTCCAACCGCTTCGTCAACGANATG
 GGATCGTACGANCCTACCGCTCGCAGGATATGTCGNGACCGNGNTCTAGANAN (SEQ ID NO. 646)

:::::::Rv75T7D3.seq:::::::
 CACTTCATGCTCGTGCCTGGCNTCGATTGCGNCAGAGNGTTAGCTCTCGAGTGNGTGACGTATCACTCCGGCNGAC
 TANCGTATCNGCTCCGCACCGGTCAACTGGTCTAGGCCACACCGGGGAGAATNCNCAGCCGNGCTATCGACCNAT
 CACGGCTTGTGCNNAAAGATAGNCAGCC (SEQ ID NO. 647)

Clone Rv76

:::::::::::Rv76SP6.seq:::::::::::

ATACTCAAGCTTCCAACCGCCACCTGCATCCGGGGCGAGCACTGCTCCGCCGACCAGTACGAACCAACCTGC GG TGCCCAGGCCATTGACAATGTGCTGGCGCCCGAGTTCTAGCACAGCAACGCCGCCACCACAGGGCG

(SEQ ID NO. 648)

:::::::::::Rv76T7.seq:::::::::::

CGGTGGTGTGCTTGGCGCGTGGTATCAACACCGCCACGAAATGGGGACAAGAAGGATTGCTGGAGCGGTGGC TGCCAAGATCACCTCGCCCAGACTGCTACGGCACTTCTACATCGAGCACACCGTGGCCATCAGTCCGGGTGT CCACACCGGAAGACCCGGCTGGCGTGGCAAAACTTGTGGATTTCGGCCCCCCCC

(SEQ ID NO. 649)

Clone Rv77

:::::::::::Rv77SP6.seq:::::::::::

AACTCAAGCTTGCAGGGTGGTGGGAGGACGTACCGCGCCGCTGTCGGTGGCGCTGGATGCCGGCCGGA TCAACCACCGCTACCTGTTCTCTGGGCCGCGTGGCTGCGGAAAGACGTCGTAGCGCGTATCTGGCGCGTGTGA ACTGTGCGCAGGGCCCTACCGCAACCGTGCAGGGGTCTGCAATCCTGCGTTCTGGCGCCCAACGCCCGGCA GCATCGACGTGGTAGAGCTGGATGCCGCCAGCACGGCGCTGGAGCAACCCCGAGCTGCGGACCAGCCC

(SEQ ID NO. 650)

:::::::::::Rv77T7.seq:::::::::::

GATGGCACTCACGCTGGACAAGACCTTCACAAAATCTGAAATCTGACCCGATACTTGAACCTGGTCTCGTGGCAA TAACTCGTTGGCGTGCAGGACGCGCGAACAGTACTTCGGCATCACGCGTCCGACCTGAAATTGGCAGCAAACCG GCGCTGCTGGCCGGGATGGTGCAATCCGAACAAGCACGCTCAACCGTACACCAACCCGAAGGGCGCTGGCCCG CGGAAACCTTGTCCCTCA (SEQ ID NO. 651)

Clone Rv78

:::::::::::Rv78SP6.seq:::::::::::

AACAGCTATGACCATGATTACGCCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTCTGGCGTGTGGTGGCC GGCCTGCCGGTGCAGGAACTGGATTACTGCCATCTCTCGCACCTGAGGTGGTCCAGGCTTACAACACCGACCCA CTCGTGCACCACGGACGGTTCCGGCCGGGATTGGCGCGCGCTGCTGCANGTGGCGAGACCATGCCGCCGANCA CCGGCATTGACCGCGCCGCTGCTAGTGCACGGCACCGATGACCGCTGATCCCCTGCAAGGCAGCCGTCGCTG CTCNAATGTNTNGGATCNGCCGACGTGCANCTGAANGANTATCCCCGCTGTNCCACNAGGTGTTCAACGAACCGG AN CGAACCAAGTG (SEQ ID NO. 652)

:::::::::::Rv78T7.seq:::::::::::

CAAGGCATAGCCAAGACCCAAAGGGATCGCAGTCACCTCCGTCAACGGCCTGGCGCCACGGTCCGTGCAGGA GACGTGGCTGCCATGCAAAGCGCCGCCCTATCAGGAACGCCCGGCTTGTGCGCTTTCTGCATCGACACATT TCCGGAGGTGTTGTGGTGGCGCANCACGCGAGACAGGCTGGGATGGCGTGCATCGTACCGGATGCGTGGCCTG AACACTGAACCTACGAGCGCATCTCGGCCAGCATGACTGTTGACTACGTCGTGTTGGCAGGGGAGTAGCGTT CACCAAGCTGGCCTTGGCCCTGGCAATGACCTGCGTTGACGACTCCGGACTAACCGCCGTANTGAGCAAGGAC AGATTCTGCGCACACCCCTCGCTGGTCGACCTTGACA (SEQ ID NO. 653)

Clone Rv79

:::::::::::Rv79SP6.seq:::::::::::

AACAGCTATGACCATGATTACGCCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTGCCTGGTGTGGTGGC CAACTCGGGGGCACCATCTCCATCACGACNGCAAACGCTCCGGCTCGCGACAGCGATCGCTGCGATNGTTG TTCGGCGGCCCTCCGGCCCTGACCCGGAAAGCCGCCAAGGTGTTGACNCTTGTGGGGTGAAGCCGATGTGTGC CATCACCGGGATNCCCGCCGCGGTCAAGACANGGATTTGCTCGGCCACCGCTCACGCCCTGANCTTGACNGCATG TGCGCCGCCGTCCTGAAGAAACCGGTGGCGGNGCAACCC (SEQ ID NO. 654)

:::::::::::Rv79T7.seq:::::::::::

CGTTGAGATCCAGCTGCGACTGTGCAAGCGCCTCGGTGGTCTGCTCGGCCTGCCGGATAACTCGTTGAGCTGGCCA GCGCGTCGTCGGCCGGATCAGCCAGCACATTGCGGCCAGGACGCCGGAGGAGACGGTGAAGCTCGCAAAGAACCTA TGGCGGACCGCATGATTACACGCGCGATCAACCACTCTGGTCAGCGCTCAAAATTGCTTCTAAACGGGCCATCG ACGGATGACGTCGAGCTGGTTAGGTCTAAACAGGTTACGAAACGATCTCGGAATTGTCAAAGGGGAAGTTAAGA AAATGGATAGATTCTACCATTCGCTGTGGACGATCGTACTTCTGCTATAGGGCTCCAGGGGATCGACACGCAACG ACCTTACCGACACCGATCCGCGTGGCGGCGAACGGCACCANGCGAACCGAAGGGCAATCCGACATCGG (SEQ ID NO. 655)

Clone Rv7

:::::::Rv7SP6.seq:::::::
 ATACTCAAGCTTATCTAGGCAGCTTGATTGGTCTGGTTGCATTGGCAGCTGCGGAGCCTGGCTCACTCAACT
 ACAACAACCGAAACAATTGCCGCTTCGGATCCAGTTCGGTTGGTACGCGGCAATGGANACCAATTCTCGGTGA
 ATCAGACTATTCTGAGTACTTGATCATCCACTCTGCACACGACCTCGAACCCCGCGCGGCCCTGGCGACCTGGAGC
 AGCTGGCGAACGTGTAGCCANATCCCAGGCGTTGCCATGGTTCGGGTGTGACCCGGCAAACGGGAAACCCCTTG
 AACAGGCCCCGGCGACATACCAAGCGGCCAAGTTGGCAACCGGCTGGCGCGTGGGAATGATCGATGAGCGCA
 CGGGCGACCTGAATCGGCTGGCATCGGGTGCACCTGTTGGCGACAAATCTCGGTGACTTCGGGTCAAGTCAGGCC
 GGCGTTGCGGGTGTCCCGAGCCTGTCCAGCCCCCTCGCTTACTCCA (SEQ ID NO. 656)

:::::::Rv7T7.seq:::::::
 CAGGCATGCAAGCTTTTGAGCGTCGCGGGGAGCTTCGCCGGCAATTCTACTAGCGAGAACTCTGGCCCAGTACG
 GATCTGACCGAAGTCGCTGCGGTGAGCCCACCCCTCATTGGCGATGGCGCCAGCGATGGCGCTGGACCGATCTTGTG
 CCGCTTGGCGACGGCGACCGGGTAGGTGGTCAAGTCCGGTCTACGCTTGGGCTTGGCGACGGTCCCAGCCTGGT
 GCGGTTGCGCCCGAAAGCGGGGGTGGCATCAGGAATGCTCACCGCCGGCACTGACACGGCAGTGGCC
 CGGCATTAGCCATCGGGACATCATGCTCGCTCATCTCGACCGAGTCGGCGAACAGCTCGATTCGGGAAC
 CCCACGCATGGT (SEQ ID NO. 657)

Clone Rv80

:::::::Rv80SP6.seq:::::::
 AACAGCTATGACCATGATTACGCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTGTAGAAAAAGATCGGTGA
 GCGCATCGATTGCTCCCGGGTTGCGCTGCGGGGGAGCTGCCGTGACCGTCTATTGGGTGATCAGATACT
 GGGCTAGTTGGTGG
 TACGTATCTCACGGCACTCAAGGAATTAAATCCGAATCGGAAACGCCCTGGCAAGCGTCAGTCCGGCAGCGCCGT
 CNCGCCAGCACCGCTGGCATGCTCACATACCACCTCGATCGCTGCGGCGANTTGTCTGCTNGCCGACCGACCGG
 CCANCCGGGGCAAACCCNGAAGACCCAAGAATTCATCACCACCATCGCTAGC (SEQ ID NO. 658)

:::::::Rv80T7.seq:::::::
 CCTCTTGACACCCACCTCGCCATCGACCTTGAGCACTCCGTCGTAGTTGGTAACATGTGACCGGCGATGGGGGG
 TGAACCGTACTGGGTGTCGGTGTGCGACGTTCATCTCACCGCGTAGCGCAGCGCTCCCTCGATCTCGACTTAA
 GCGAACCCGAGCCGCCGTTGAACACGAAATCNAACGGCTTGGCGTCNGCCGGCAGCGAGCTGGCGCCACCT
 GTTGCCTTGGCAAGGATGTCNGGGGAANCTTGACGTTGCCGGGCTTGTANACCCATGCACTGTTGGCAACGT
 CGGCCAGCAGNTATTTGCCGTGTCACCGGCCCGCCTCGATGGTTTCTCGAAGTCTCCGGTGGTGTACA
 GCTTCTCGTTGATCTCGTTCGCCAGCGCGCTCTCGCCGCGACG (SEQ ID NO. 659)

Clone Rv81

:::::::Rv81SP6.seq:::::::
 AACAGCTATGACCATGATTACGCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTGGAAAGGAGATCCCGGG
 AACCTGGTGGCAACCCCGCCATTGGGTTGTTGGATTGCCGATCAGCGTAANGAAAAGCTCGTCTGGAGACAGCGGG
 TCGGCCGAAGCCGCAAGATTGGCCATCACTAGTGACGANATCGTGGCGCTCTGCGAGTANCCNAAGACAGTGA
 TTNCGGCGCAATTGCTGCCGAATCGCACTTGCAGAAATGACNGCACCGTGGCCACCGANGAATCNAAGTGAGG
 TTCTTGATCACGACCACCGGGTNGAGCCCTGGGGCGTGAAGANCCTGCGNATAACACCCGGGACGCTGCCACTC
 ATGTNCAGCGCGTTCGCGANCTCNACATATCT (SEQ ID NO. 660)

:::::::Rv81T7.seq:::::::

TCCTGGTATCGANGGCCGCGGTTCCGGCGAAAATCCGGTTGGGTTGGGTCGGGTTCAACTTGANCCTGGTCC
 GCAGCTGATTACCGTGGCAACGCCGGCCAACCTGCGATAATGCGCATCCGAACCCCTCACCGCCGCCGCGATCA
 CCCAACCTGATCCAACGACAACCGCCCCCTCCCGCATACCCGGCGAGCGCGGAAACCTCCGGCAACCGCCGCGCCA
 CGTGGCGATCGTGTGGCGTGTGCGTACGAAACANCCATCTTCCAGGCCACCAACCCGCCACCGACCGCGCCCCCG
 TCACACCCACAACCCGTCGCGATCCAGCTCAGGCCACGATCTCCACATGCGCCCATCAATCGCATTGCGCTGAACGG
 GCAACTCCGCGAACCTCCCAA (SEQ ID NO. 661)

Clone Rv82

:::::::Rv82SP6.seq:::::::
 AACAGCTATGACCATGATTACGCAAGCTATTAGGTGACACTATAGAATACTCAAGATCTGGTACCCATCCGTGATA
 CATTGAGGCTGTTCCCTGGGGTGTGTTACCTTCCACGAGGAAAACACGTAGCCCTTCAGGCCAGATCTGAGCAAG
 ATGAACAGAAACTGAGGTTTGTAAACGCCACCTTATGGGAGCAACCCGATCAGGGTGGAAATACGTCTCAGC
 ACGTGCAATCGCGTACCAAACACATCACGCAATGATTAATTGTTCAATTGTATAACCAACACGTTGCTCAACCCG

TCCTCGAATTCCATATCCGGTGCCTAGTCGCCCTGCTTCTCGGCATCTGATAGCCTGAGAAGAAACCCAAAC
TAAATCCGCTGCTTCACCTATTCTCCAGCGCGGGTTATTTCCCTCGCTCCGGCTGTCATCATTAAACTGTGCAA

(SEQ ID NO. 662)

Clone Rv83

:::::::Rv83SP6.seq:::::::
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTANCGCCACCTCCGGCG
GAACCTCCACGGCGTGGATNAAGGTACCGCCGGATGTTGCCAATGGCAGGGTGTGCCCCTGCTGANGTCGCGTT
AGCGCCGGATTCCACACATCCCCTTGCAGAAANTCCGGTGGGTCATGATGTNNCGCTTCTCCCNCTCNANATAATG
GANCAACGCNATCCGTGCCGTACGGTCTGGGTCNTACTCCATGTNCGCACCTGGCGTTGANACCATCTTGTCA
GCGCGAAAGTCNATCATCCGGTNAGCNCNTATGANCGCCCTTGTGCCGGTGGTAATCCGGCATGCGNTT
GCGTCCACCGCGAACGTGCAACGGGGCNCCAAGANTTCTCCNGGGTTGAACCGGTNATC (SEQ ID NO. 663)

:::::::Rv83T7.seq:::::::
TGTGTGTGGTGGTAACCCATCTGAGCAGTGTGCCAACCGGGCAGCCAGCTCCAAATTGACGTGAGCCGCTCACTT
GCTGGGTAAGCGTCG (SEQ ID NO. 664)

Clone Rv84

:::::::Rv84SP6.seq:::::::
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATANAATACTCAAGCTTGCCTGNNATNGCCTTGGT
CAACGGCACCGTGATCGGATCNGGTCTACCGCACACATNGACTGGAGCTTCGGCGAANTCATCGCCTATGCCCTCGCG
GGGGGTGACGCTGANCCNGGTGACNTGTTCTCNGTCNGGCACGGTCCCCACCTGCACGCTCCTCNAACACCTCANGCC
ACCGGAATCATCCCNGGTGGCTGACAGANAGCAGANNTTGTGNCCTCCAAGTCTAAAGGCTGGCGANANAAGCAN
AACGTCCCACNAACGGCACTCCTTCCNTTGCTCTC (SEQ ID NO. 665)

:::::::Rv84T7.seq:::::::
GAAATCATTGATGGTTGAGTCACCAAGGCCGATCAAGCCTTCGCCGAGCCAATTCCAATCAAGAGGCCAAGCCCGT
ACCAATCAGCCGGCAACGAGGGATTCCGTATTATCAGCCAAATAACTGCTCTGGGTTACACCCAAACAGCGCAA
TATGGCGAAAACGGTCGCCGTTGACGACATTAAATGTACGGTATTGTAGATTAAAAGATAACCCACCAACAANGC
AATCAAACGTGAGAGCGTTAAATTGACCGTAAAGCGTCCGTCATCTGTTGACNGTGTCCCCTGGGTATCCGACGT
TTCCATACGCACACCGGCCGGCAGTCTTGTGATGCGTNNTGCAATGGCTCATCTTGATGATCAAATCGATGNT
GCTCAGTCTCCGGCATATGAAACAACTCTGGCCGTGAAATATCAGCAATGATA (SEQ ID NO. 666)

Clone Rv85

:::::::Rv85SP6.seq:::::::
CTTCGCCAGGCCGGCGCGGATGTCCTCATCGCTCACGAAACATCATCCGAGCTTGACGCTGTCGCCAACAGATCC
GCCGTGCCGGCGCCGCCACACCGTTGCCCGATCTGGCCCATCCGAGGTGACCGCCAGCTGGCTGGTCAG
CCGTGGAGCTTCGGGAAGCTCGACATCGCTCAACAAACGTTGGCGCACCATGCCAACACGCTGCTAACGAC
CGACCAANGACCTCGCGACGCCCTCGCCTCAACGTGGCACCGCCCACGCGCTGACCGTCCGGCGGTGCCGTGA
TGCTGGAACACTCCGGCGGGCAGCGTGATCAACATCAGCTCCACCATGGCCGGCTGGCGCGCGGGTTTC
(SEQ ID NO. 667)

:::::::Rv85T7.seq:::::::
TGTGGGCTCCGATCCGGCGCATGGCATCGACGGCGACGCCGATCGATGACGGCAGGTTACGAGCTTGAGGGTGT
GAAGTTGTGGACCAACCGGTGTGGTAGCGGACCTGCTAGTGGTATGGCGGGTACCGCGCAGTGAAGGGCNCCG
AGGGGGAAATCANCGCCCTTGTGCGTGGCTGACCGGCTTCNTCGCTCAGGGTCCCCAAAGACAACATTGATCGC
GCGTGGCATCGAAAACGGCGTGACCCGGCTTCNTCGCTCAGGGTCCCCAAAGACAACATTGATCGCANGGAAGCGAC
GTCTGAAGATCGCGTGAACACACTCAACGCCGGACGGCTGTCCTACCGCGATCCAACCGGAGT
(SEQ ID NO. 668)

Clone Rv86

:::::::Rv86SP6.seq:::::::
GAGCTGGCCGAGCTGGACCGGTTACCGCGGAACCGCTCTCGCTCGACGACTTCAGCAGCGGGCTTGAGCGCG
CTGGAAACGCCGGCCACGGTGTGCTGGTGTGCGCGCCGACCGGGCGCTGGCAAGACAGTGGTGGCGAGTTGCCGTGCG
CTGGCGCTGGCGGGCCGGAGTAAATGTTCTACACCAACGCCGCTGAAAGCCCTGAGCAACCAAAGCACACCGATCTC
ACAGCACGCTACGGCGTGACCGAGATCTGGCTGACCGGGTACCTGTCNGTCAACGGCAACCGCCGGTGGTGA
TGACCAACCGAAATGCTGCGAACATGCTCTAC (SEQ ID NO. 669)

:::::::Rv86T7.seq:::::::
 GATCTCTGGATCGCGGGGCTCTCGGGCGCTCGGCACCTCAGCGGGCGCCCTCCGGCCGAACCATTCCT
 AGCCATAGATGACCGCACCTCGATGCACGGTTGGCGAACCGCGAAGGCGTCNGTCGGGCCCAGCCGGCAATG
 CGGGTACCCGGGAGCGCGGGTCNGTANACCANCCTGGACTGCCTCGCGGGTGCCTCNAACNTCAAAGTCCCCGGCGT
 CCCATATCGCGTATGACCGGGCGCCCGACCANGGGTGCCTCGGCGTCTCGAACACCACCGGGCCGCCAG
 CCGCCGCGGGTCCGGCAGCNAACCCGCCGCGCAGTACCCGCTGCCCGTGCCTGATTGACCGCCGCGCAGCCT
 GGCCANGGATCAAAGCCCGT (SEQ ID NO. 670)

Clone Rv87

:::::::Rv87SP6.seq:::::::
 GGACCGTAGCCCGCCAGGCCGGTCAGGTGCCCTCCAGTCCACGCCGCTGTGGTCGGGAACCGCTTATCTCAAT
 CGAGACGATGCCAGCTTCATCGTGTGGCGATCTTGTCCAGGGCACCTCGAACCCGGCCTGCGAGTCAGCAGGCCACGC
 GATCGTGTGCCCTTCGGCTCGACCATCGTCACTCGAACGGCAGTCAGTGGCCAGCCGTTGGC
 AACGACCTCAGANGCAGGATTGGACATCAGCCCTAGCCCGCTCGAACGGGACGGTCACTGGCCGAGCCGTTGGC
 GGCAACAGACAGCACCCAGCCAGCTTCAGAACGGTATCGCGGCCGGAAAGCGCTCGGGCATCGTNCTACAGTAGC
 GACCTCCTGTCACTCCACGTGCCGCTCGTCCATAGAATCTTCGCCGGCGGGTGAATCTCGNNGATCGGGGCN
 GGC (SEQ ID NO. 671)

:::::::Rv87T7.seq:::::::
 GCTCGTTGCCGGCGGCGATCTCGTCAGCTCGTCTTCATGCCCGGGTGAAGTCGTAGTCGACGAGCCGACCGAAAT
 GCTGCTCGAGCAGACCGTTACCGCGAACGCCACCCATGACGGCACCAAGTGCAGTCAGTGCCTCTGTGCACGTCAGGCC
 GATCCTGGATGGCTTGATGATCGACGANTAGGTCGACGGCGGCCATGCCAGCTCTCGAGCGCTTTGACCAGCG
 AGCCCTCGTGTNNCGGCCGGCGGGTTGGTGGCATGGCGTCTGGGTCAACTCGACNATGTCACCGTTGACCCG
 GGGTCAGATGGGCAGTCGCCGCTCGGCATCGTCAAGCCTCGCCGTCAGCTCGCCG (SEQ ID NO. 672)

Clone Rv88

:::::::Rv88SP6.seq:::::::
 GTCTTCGATGGCTGCTCTTCGGCGCTGACGCTGGCGATCTATCACCCCCAGCAGTTCGTACGCCGGAGCGATGT
 CGGGCCTGTTGGACCCCTCCCAGCGATGGGCTCCACCCCTGATCGGCCGATGGGTGACGCTGGCGGTACAAGG
 CCTCCGACATGTGGGCCGAAGGGAGGACCCGGCTGGCAGCGAACGACCCGCTTGAACGTCNGGAACNTGATCG
 CCAACNACACCCNCCTCGGGGTGACTCGGGCACNGCAAGCCGTCGGATCTGGGTGGCAACAACTGCCGCAAGT
 TCCTCGAGGGCTTCGTCGGGACCATCAACATCAAGTTCCAAGACGCCAACGCCNGTGGCGGCCACAACCGCGTGT
 TCGACTTCCCG (SEQ ID NO. 673)

:::::::Rv88T7.seq:::::::
 GCCAGGTCGAGGTCCCATGCGCTGGGCATTGATGCTGATGCCAGGACGTCAAANATTGGTCCGGCTCAGCTGG
 GCGAAAACGTGGCCCCAGGACTTGCCTGGAGCTGCCGGACTGCCGGTCCCGTCCGGCAGCTCGGCCGGGGTCAGAAA
 AAATTGCGCCAGGTGCAACTCCCGCCGTANGCCAGCTGCTCCAGGGTGTGGCATAGAGCCCGGGCCGAGCG
 TGCTCGCTGTCGGCAACACCGCATGGTCGAGAACGGCTGCCGCCAACGAAATCACCTGCGTCNAANGCTCGCG
 GCCAACCTCAGCACTCGTCGATG (SEQ ID NO. 674)

Clone Rv89

:::::::Rv89SP6.seq:::::::
 NAAACGTTCCGGCTTNGGTGCCGGCGCTTATTGCGTCTCTGGGATCANCCTCAGTCGCCGGCTGCCGTTGGG
 TATNANTTGCACCGANCAGGAAAATCCGCACNANAATGCGNACTAGCGGCCTGCGAGAANTGCACTCCTCGCGAACNCG
 ACTACCGGGTGGACANCACAAGCCGCCGAACACGCACTGCCGGGGATNGGCTCTATCGGCCGCCGTC
 AACTNGGAACAGACAGCTGCGGTTCTACCGTGATCTGGTGGGAATGCTCNACCANACCTCCCNANNCTACGGAACNA
 CGCGCGATATTGCGTCCGACTN (SEQ ID NO. 675)

:::::::Rv89T7.seq:::::::
 CGAACGACGAACNCCNAAGCCATGGTGGCGCGTCAAAAGGTCGCGGTGCCACTACTGGAAAATGCCCTTG
 AGCGTCNCTCGACCNCCGCCCTCGAGTTGGCTNTAACGAAATACCTGATGCCGATCANGTCNAACGTCTCCGTCGCNN
 AACGTGCAGCGGCACCACTCTACNANGTCTCGGTNCCGCCAGNGCACCACCAAGTGCACNAATCCNTGCGCC
 NTCGGGCCAGCANTCCGGTGCNACCGNGGGTGGGTCCGGCAGTGGTNGGGTGTCTCNNTACNGGAACGCCAGCGCN
 ATCANCATCGGCANACTCNGCTCGATGTGCCGGCGAACCATCCCCCACAATGATCNGGTGCGTCTGATCAGGCN
 (SEQ ID NO. 676)

Clone Rv8

:::::::::::Rv8SP6D.seq:::::::::::

TTAGGCGTGACGGCCACCGGGGCCACTCCGACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTC
GCCGACTTCCCGCGTACCGCCTCAACTTGTGTCGACCCCTCAACGCCATTGCCGGC (SEQ ID NO. 677)

:::::::::::Rv8T7D4.seq:::::::::::

CGTCACCCCGATGCGCCCAGATCGGGCTTCGAGATAAAGCACGAACCTGGCGGGCAAAACGTGATCTCGGAGCCGG
AAGGGCAATCAGCGACCGTCGACGAACGACACCGCGAGACCACTTAGGCAGTGACGGCCT

(SEQ ID NO. 678)

Clone Rv90

:::::::::::Rv90SP6.seq:::::::::::

CTTTTCNCGATGTCTCATGATNCCNANGAGAACNNTGCNANCNCNGCCGCTGACNTNGNCACCGCTNTGGCNGNG
TGACATTGGTGGTGGTGGGGCTGCNAACGCCGACTCGANGCCGANCATNTNTTGCACCGCCTNTCGTCTC
NACCGCANNCCNATCTCNGCCGNCACCGTGGANCTACNGCTNCTGCCATCTCGCCNATGGCTCCNGCENN
GCNCAACGTNTGGTTGGTNACTGCCTACCTGGCTNT (SEQ ID NO. 679)

:::::::::::Rv90T7.seq:::::::::::

GCTGCGCCAGTCGTTGGTGGCGGTATGCCGTTGGACCNACCACGGAGTTAGTTGCCGAACCGCGGACCACCGCAAG
CACCCGGTCCTGGTCGCGCACCGCGTGGCCAACCGCTTGAGCACCACCGCCGAGCCCTCGCCGCGACGAATCC
ATCCCGCGTTGGCGTCNAANCTGTNGCATCGGTGGTGGTACAGCGCCGACCCACTGGACAGCGCGATGGCGTGA
CGGTNANTAGGTGACCTGCCNCNCACCGCCAAATGCCACCTCCGCTCACNCATGCAATGGTCTGACACGCCNAG
TGAATTGCCACCGAGCACAACAAAAATCGGTATCTCNGCAGCGGACACGCNATCCNACTGATACTCGATCCGC
CCCACCGCTTGNANCTCGGGTTCCNGTGCTCATGTACCNCTATGTCGGTCTGCGCNCGATATTGACGATCGTGTTC
CCACGANNANAGANCCTCATCACGCCGTTGAGTGC (SEQ ID NO. 680)

Clone Rv91

:::::::::::Rv91SP6.seq:::::::::::

CTGTGTGCGGNGCGCGCATATCGGCTTTTACTAACCGAACCGATGTGGCTCCGATCCGGCGCGCATGGCATCT
ACNGCGACGCCGATCGATGACGGCAGGCTTACGAGCTTGAGGGTGTGAANTTGTGGACCNCCAACGGTGTGGTAGCG
GACCTGCTANTGGTTATGGCGGGTACCGCGCAGTGAANGCACCAGGGGGAAATCANCGCCTTGTGCTCTANGCT
GATTCTCCCGGGATCACNTGGAGCGCNCNCNANTTATGGGACTCGCTGGCATCCAANACGGCGTACCGGCTTC
TCCNTCNGGTGCCAAAGACAACCTGATCNGCNGGAAGCGACGTCTGAANATCGCGCTGATCNCACTAACGCCG
ACGCTGCTTACCGCGATCGCACCGGANTTCCAANCCGCGTNANNATCGCGNAATGNCCGTCCACNANTGCAT
GG (SEQ ID NO. 681)

:::::::::::Rv91T7.seq:::::::::::

TGGGGTGCCGGCGCCGAGTTGCGTCCCTGGGATCACCGCAGAGTCGCCGGCTGCCGTTGGCTATGAATTGCA
GAGCCGGAAAATCCGCANAAAATCGCAGTACGGGCTGAGAAGTGCANCCCTGGCGAAACGGAGTACGGTGGACA
ACGAAAAGGCCGCCGACACGCACTGGCCGAGGGATTGGCGTCAATCGGCCCCCGCCGTCGAACCTTGAAGANAC
ANTGCGGTTTACCGTGATCTGGTGGGAATGCTCCAACNNACCTCNCGAAAGCTACGGAAGCNACGGCGCATNTT
CGGCTTCCAGCTGACCTGACGCTGGAAATCG (SEQ ID NO. 682)

Clone Rv92

:::::::::::Rv92SP6.seq:::::::::::

NGGCGNGGAAGTTAATGCCCTACTGGTTCNATGCTCNCACNTCNCNGTGACNNCTGCNCCGACCCGCCAGGTCC
GNCCTGNNACCCACCGANCNGCGATCGGGACTCTNGTACGCATCCAACANNGANCAACGTGCAACGGGGAGTNGTNC
CGCCACTTCGNCNATGACGGGGTCGATCCNTCGACGTCCGCGCGTCGGTCAAGTGGCGGTACNCTCCNGTA
CTCGACCNCACNGACGAGAGGAACCGANCCCATCTACGTGAGCAACANATCTCTGTCACCGACTACACCAC
ACCCAGGCCATCGCCGNCACCGCAGNGCCCTCGACGCCNTACTGGTCCNGNGGGCGCTCCGGTTGTCTNN
NCNTGNCGTGTTCTTCACNCACGCCNACATCGANCCGAGCNAATNCNANGTCCGTCAATC (SEQ ID NO. 683)

:::::::::::Rv92T7.seq:::::::::::

GGACACTGTTGCGTGCCCCCTCGTCAAAGCCGGAGTGGTGTGCTGCGCCGGACCCGACCCGACCTTCAGGGGGTT
CACAGCTCCGTTGGGATCTGGCTGGTGGCGGAACCGCAGTTATGTCNGCTACGGGCGCCGGACTCGCG
GACTTGGATCCGGTTCGGGATCTGGCTGGTGGCGGAACCGCAGTTATGTCNGCTACGGGCGCCGGACTCGCG
TGGCCTTCCGGCAAGCNCNANANAACCGCAGCCGGAGGTGTGAACTAGCTTCGCGCGTATTTACAAATTGCTTATA
TGTCTACACATAAGACGCAAACGTCTATTGTCACANTCCANCCTGGTGTGGCNATGAAGATGTTGG

(SEQ ID NO. 684)

Clone Rv94

:::::::Rv94SP6.seq:::::::
 TCCCTCTCGGTATCGGTTGGGCTGTCACCANCAGTTGGTAGTTCTCACGTNCTGTTGTCAGCGTCNAGCCGTC
 CGCGTGTNANGTCNCGGACCGTATCCCGCAGGCCGGTCANGGTGCCCTCCANTCCACGCCGCTGTGGTCGGCG
 AACGCTNATCTCAATCGAGACCATGCCAGCTCATCNGTGTGGCAGTCATCNGTGTGTCNNACGGCACCTCNAACC
 CGCCGCTGCACTNACCTCGAGGCCATTGGACATCANCCCANCCGCTGCGAACGGAACGTCAGCNCNCTGG
 CGACAACCTGCCAACAN (SEQ ID NO. 685)

:::::::Rv94T7.seq:::::::
 CACNCCGATCGCNAGCCCCNNTAGAAATNGTGAAGCCAGTTGGTGCAGCGCTCGTTGCCGGCGGTNATCTCGTC
 GCTCNCNTCCATCGCCCGGTGAAGTCGTACTCGACNAGCCGACCNAAATGCTGTCNAGCAGACCGGTACCNNA
 ACNCCNCCTCNGTACNGCACCAGTGCNCCTGCGTACCGCAGTCAGTACCCGCNATCCTGGATGGTCTTGATGATC
 NAC TANTNTGTCGACGGCGGGCGATGCCATCTCTCNAGCCGTTGACCAAGCGACNCCCTGGTGTATCGGGCGGG
 TTNGTGGCATGGCGTCTGGGTCACTCNACNATNTTCANCCGTTGACCCGGGGTCACA

(SEQ ID NO. 686)

Clone Rv95

:::::::Rv95SP6.seq:::::::
 TGGCCTTCTGNANCAGGGCNNACATNGCTATNGCGAGCGTGTAAACCGATCATCNCNGCGACTGTGGCCTGANCG
 GCAAGGGTNGCCTNATTCTCCTCTGNGCATGGTNCCACACGGAATGNCGTTAGTCTGGTCGGCAACCTGGCC
 GCTGCGGGTGGGTTGGGATTCGCTCGGCTANTAAAGGTGTCGCCTGGTGTNACNACTAATCNCNATATA
 NCCTTANC GGGAGTNGCCTCCGATCCTNGCCCTGCCGNGCGATCNCGTTGACNACCCGACCCGAACTCNC
 ACNGCCTACGCCATCTCCCCGGATTCTCGCGCNGNTNCCNGGGACCCGGACTGTGACNGCCCAA
 CGGCTCATCATCG (SEQ ID NO. 687)

:::::::Rv95T7.seq:::::::
 CCGGATAGCGGTGTCGAACTTCGCCGTTCCCTCANCAGCATTGAGCTTCAGCCGACCGGAGGTNNGAGTC
 ATCGGGTCCTCGCCCCGACCCCGCTGGCTAAATANCCACCCCGAGCGCGGTACGGTCTTGACCGGGACGAC
 ATACCGGCAGCGCAACATCNCGCCGGCTGCAGCNTGAACGTCCAATACCANTCNAACAGTGTCCGCG
 GTNAAAC CCGANCCGGCGGTGCGTTCTGTAATCAACGGCTCCTCGCAGCTGCAAGTGC
 CGCGTCCGGTGCACGGACTGTGACNGCCCAA (SEQ ID NO. 688)

Clone Rv96

:::::::Rv96SP6.seq:::::::
 CCTCCCGACCACATACAGGCAAAGTAATGGCATTACCGCAGCCATTACTCCTACCGCGCAATTAA
 CGAATCCACCA TCGGGGCAGCTGGTGTGATAACGAAGTATCTCAACCGGTTGAGTATTGAGCGTAT
 GTTTGGAATAACAGGCGCAGC GCTTCATTCTAACTCTCCAGCGTGGTTAACAGACGATCGAAA
 ATTTCATTGCAAGGCACCAAGTTGAAGAGCGTTGATCAATGGCCTGTC
 AAAACAGTTCTCATCCGGATCTGACCTT
 ACCAACTCATCCGTTACGTACACATTAGAACCATGCTTCCCCAGGC
 ATCCCAGTAACTTGTCTCCATCCA CGGGACTGAGGCCATTACTATTGCTGATTGGTAAGCAA
 ATACG (SEQ ID NO. 689)

Clone Rv9

:::::::Rv9SP6.seq:::::::
 CTTCACNTCCGTACGGCTCGGGTACGCTTCTGGTCNCATTGTGCGAGTGATAGATGACGACCGG
 ACCTCGTCGGCATTGCTCACCGGAATCCAACCGGTANAAGGT
 CGCGTGCNGCATTGGTCACTCGCAGGCTTCGTCGGGTGGTC
 CGCGACCGCATGGCACCACATCGCATTCA
 CACCAAGGTCTGCCGAATCACCAGCACGTANACGGT
 CTTCTCTTAAGCAACACCGA
 ANTTCAAGGACCCGAATGCTCCGGAAACATGT
 ACGGTAGGTGGTATTCCGGTACCGGCTGANCATTGAGCAC
 CGGCCAGCACCACGACACCAGGCAATCAGCCGCC
 ACCCGACCGCG (SEQ ID NO. 690)

:::::::Rv9T7.seq:::::::
 CAGGGCATGCAAGCTTGTGCGCCGAAACCGAGCGT
 GAGCACGCCAGCCACGCCACCGCGACACCACCCGG
 CTGCGCTACGTGAGGCATACCG
 GATTTGCGCATCCGC
 AGCCGCACCC
 TGGACGACAGAACCGT
 GCGCTACGAATTGCTTGTGCGGGGG
 CCAAAGAACAGCTTGG
 GATCTCGGC
 CGGATTGGCCGGCGCGCTGGTC
 CGCCAAGGAAGACCCGTT
 CCGGTGCTGAT (SEQ ID NO. 691)

Table 4 : End-sequences of the polynucleotide inserts cloned in the named recombinant BAC vectors contained in the I₂₀₄₉ *M. bovis* strain Pasteur genomic DNA library.

RvXXXSP6 corresponds to the SP6 end-sequence of the clone RvXXX.

RvXXXT7 corresponds to the T7 end-sequence of the clone RvXXX.

RvXXXIS 1081 corresponds to a region located close to a copy of the IS1081 repetitive sequence (Insertion element).

The character « - » denotes an uncertain base residue.

Clone X0001

:::::::::::::::X0001SP6.seq:::::::::::::

AAG-

TCGGGTTTCCACACGCGCGTTGACCTAGTCATATGTAATCATGTGTACCATGTGCGGGCGCTTTGACGGCG
CGAACCAACCGGA-ATTTCTGTGATTCACTGCATGCGTACCATCTGGCACAATTGAGCA-TTGTCT-
TCGCCTGGTCGG-CGGTTGCGTGCCTGCTGCGA-ATGCACCA-
TAAGCCCAGACCCACCAGCCTTGGTGACCACCGCACGCTGCGTGTGGGGGTAACCACCTCCGCACCCCAAGGATGGT
CATTTCCAATGAACCGGCTGGACTTCGTCCA-A (SEQ ID NO. 692)

:::::::::::::::X0001T7.seq:::::::::::::

GTCGCGGTTGATCGACCGATCTCACCTCGTAACCTCGATGCTTAGCAGGATCCAGCTTGACCGCGTTGGCTCT
ACCCACTCTTGAGTGGCGCGTCGCGCTGTGCCCCATCGGTGTTATGACGAACGCTTCGAAAGACTCCCTCTTGTG
AGCCGGAATGTCGCGTAAAGAAGTCCATGTCGGGAAGTAGACCCGGTGCCTCCACGTGGTACTCCCTCGAGG
TCCGCTTCTCGCCGGATCCGATAAAACACCGGCCCCAGGCACCGCAGCGTGAAGTTGACCGCTCAGGTAGGTGTC
ATGCGCGGAGCTCCGGAGTGCAGAGAAATAGCGGTGCGGGTAGCTGTAGACCGGATGGTTCCGCCCCAGGCTGACG
TCGAAGATGCCTCCTTGGAGGGCGCGA (SEQ ID NO. 693)

Clone X0002

:::::::::::::::X0002SP6.seq:::::::::::::

AACTCAAGTTTTACGGTGAATCGCGCATCACCTGGTTATGAACTGGAAGCAGCGCAGCGCTCCTTTGGCCGCA
ACATGAGCCAGCCTCTCGTCGGCGGTGAGGTGCTCGGCAGCTCGGCCGACAGCCGCTGACCCCTGAAA
CCAGCTTCCATATCCCGCAG-
AACGACGCCAGTCCGTAACCTCCGCACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGCCGG
TGT (SEQ ID NO. 694)

:::::::::::::::X0002T7.seq:::::::::::::

GTCGAGGTTGACAATGTGGTGCCTTCGGCGTACGTGCATCGAGACACTGGCGCA-GCTATCGCACCCGGT
ATCGGCTCGAGCAAATCGGGTATCGTTCTGAGCATGAGTCGGGACCGTGTATGGTCGACACCCACGACGG
AAAGACGAGATCGCCGTCAGCATGTGTGCCGGATTATCAGGACTGACCTCTGGTGCACGGGATGTTGGTC
GGATGCCTGGCGCCGGCGTGGTGTGGCTCGGCTGGATAGCGAGGTAGCGAATTCTCGTGGCAGCTCGAA
AGGGTCCCTGCCGGTGCCTG (SEQ ID NO. 695)

Clone X0003

:::::::::::::::X0003SP6.seq:::::::::::::

TTCGAGTCATCGGCCGCCCTGACCAAGAA-ATGCACGTCG-
GGTTCGATCGACCCGATCTCACCTCGTAACCTCGATGCTTAGCAGGATCCAGCTTGACCGCGTTGGCTCTACCCA
CTCTTGAGTGGCGCCGTCGCGCTGTGCCCCATCGGTGTTATGACGAACGCTTCGAAAGACTCCCTCTTGTGAGCCG
GAATGTCTGCGTAAAGAAGTCCATGTCCGGAAAGTAGACCCGGTGCCTCCACGTGGTACTCCTCGAGGTCCGC
TTCTC (SEQ ID NO. 696)

:::::::X0003T7.seq:::::::
 GTCATGTGTACCATTTGGGGCGTTTCGACGGCGAAACACCGGAGATTCTGTGATTCACTGCATGCGTA
 CCGCTGGCACATTGAGCAGTTGCTGCGCGTGGTCGGCCGGTTGCGTGCGAGATGCAACAAAT
 AAGCCCGAACCCACCGGCTTGGTGACCACCGCACCGTGCCTGGGGTAAACCACGCCGACCCCAAGGATGGTC
 ATTCCAATGAACCGGCTGGACTTC-TCAACAA (SEQ ID NO. 697)

Clone X0004

:::::::X0004T7.seq:::::::
 AACAGCGCGGTTGAACTGATAGGTGCGGCCCGGCTCGAGCAGGCCGGCCATTGTTGATGCGGTTACCGAAAGAT
 CTCTTCGGTGACCTGCCGCCGCCAGCTCGGCCAGTGCCTGGCCGGTTGGCCGCCGGCAGATCTTGGCGT
 CCACGGTGGTGGGG (SEQ ID NO. 698)

Clone X0005

:::::::X0006T7.seq:::::::
 GCATCTGGCTGGCGGTGGTCGCGCTCCGAAGCGTCGAACACCATGCCAGCGGGCTTCCACATCAACGACCA
 TTTCGGCCAGCTTGCAGGCCATCAGCGCTTGTGATGAGCGCCCCACCGAATGCCGCCGCTGCCGGCGTA-
 CACAGCATTGACCAAGCGCGGGCGCTGCCAGGGCGAACGAGCGTGCCTGCCAACCGCAATCTGTTGGTCAG
 CTCCATCATGCGGGTGAGTCCCTTGGCG (SEQ ID NO. 699)

Clone X0007

:::::::X0007SP6.seq:::::::
 ATCGGTTTCCAGCAACAGCCGATCGACGGCTCGCCCA-
 GGCGCCTCCGGCGACCCGACCATTGCTGCGCCGCTAACGCCATACGGATGACGCGCAGTCGTCGCTGTCTA
 GCTCCACCATCGCTGACACCGGGGCCAG-ACCCATTGCCGTCGACTCGTA-
 AGCAGGTAATCTCGTCACTCGGACTCGTAACCACCGCCGCCAGCTCCGCTGCCAGGTGCGGGGGTTGACACCGGC
 GGGCATGGGATGGACGACGACGCGGTGCTGACGGCGCTGTC (SEQ ID NO. 700)

:::::::X0007T7.seq:::::::

AGCGGTTTCCA-
 GCGGGATGTGCTGTGAGCGCCGACCAACAGCGCCAGCCTAAGGATGGAACGCACGGCATCTCTGACCGTAACC
 GCGTTGTGATCGCGAGCTGAGGAGACGGTATGGGGAGGGTCTGGAGGCCATCTGGATGTTGATGTCGAT
 CTTGAGCCGGTGCAACTCGTGGCCGGACGGTACGCCGACGGCGAACGCCGCTACCACCGTGAACCTTCTGAGGA
 AACGCTCGTTGGCTACAGAGATGATGGTGGTACCCCGAGCTGGATACCGAACCTCGTCAATCTGCACG
 (SEQ ID NO. 701)

Clone X0008

:::::::X0008SP6.seq:::::::
 CAAGCTTCCACAGGTAGGGATCGAGGAACAGCGCGTTGAACTGATAGGTGCGGCCGGCTCGAGCAGGCCGATT
 TGGTCGATGCGGTACCGAAAATCTTCGGTACCTGCCGCCGCCAGCTGCCAGTGCCTGGCGTTGGC
 CGCCGCCGCAACGATCTGGCGTACCGGTGGTGGGTGATGCCGCCAGGATGCCGAGCGGGCGGTGAGCC
 GGGTGAACTTCGTCGAAGCTTGACCCCTGCCGCGGGAGGGCGAACACGGTGGCTGCGTANCTCCACCAAGCCCG
 GCAACCTCGGGGGTGGCGCC (SEQ ID NO. 702)

:::::::X0008T7.seq:::::::

TGGACCTCATGACAACCGGGCGATTACCCCGCTACCGCCAGCAGCATGACGGCGTAGCGAACACCGCCGGAT
 GCAGCGCAGGTGCGTCGATGTGCTACCGAACGCCGCCAGCTCGAGGATCACCGATGCCACCCCTG
 AGCGCAGACCCGACGATCCGTACACCGCCACGCCGATCAGGCCCTGGCCAGCTGGCTATATGGCGCGATGGT
 AGATGGCCAGCGCACATACATTGTCGGCGCAGAACACGGCTGGGGCGGGTGCATGAAACACTAGGCACG
 CAGATGCCCGGGTCAACAGGTGACCATCAGAAAGCCTGCG (SEQ ID NO. 703)

Clone X0009

:::::::X0009SP6.seq:::::::
 TTTGGTGCGGCCGGCAATCAACTTC-GCTC-
 CAGCGGTTTCCCAGGGGGATGTGCTGTGAGCGCCGACCAACAGCGCCAGCCTAAGGATGGAACGCACGGCATCT
 TCTGACCGCTAACCGCGTTGTGATCGCGAGCTGAGGAGACGGTATGGGGAGGGTCTCGGAGGCCATCTGGATGT
 TGATGTCGATCTTGAGCCGGTCAACTCGTGGCCGGACGGTACGCCGACGGCGAACGCCGCTACCCG
 GACCTTCTGAGGAAACGCTGCGTTGGCTACGATATGATGGTGGTACCCG (SEQ ID NO. 704)

:::::::::::::X0009T7.seq:::::::::::::
 CGCCCAGGGCCGCTCCCGGGCAGCCATTGCTGCGCCGCTAAGGCCATACGGATGACGCGCAGTCGCTG
 CTGCTAGCTCACCATCGCCTGCACACCGGCGGCCAGGACCCATTGCCGTCGACTCGTAGAGCAGGTAATCCTC
 GTCGACGGACTCGGTAACCACCGCCGCCAGCTCCGCTGCCAGGTCGGCGGGTTGACACCGGGCAGTCGGATGG
 ACGACGACGGGTGCTGACGGCGCTGCGACGCTGAGCTCGGACACAGCTAGTAAATGTAGCCTAACCTACTTA
 ATGGGTCGAGCCCCCCCCGGGTCGCTGCATGTCACGTTGCTGACTGGAAGAAAATGCTCGTGGAGCAAATG
 GCACC (SEQ ID NO. 705)

Clone X0010

:::::::::::::X0010SP6.seq:::::::::::::
 AATACTCAATCTGATCGGTTTCCAGCAACAGCGATCGAGGCTTCGCCCAGGGCGCTCCCGGGCAGCCGACCA
 TTGCTGTCGCCGCTAACGCCATCACGGATGACGCGCAGTTCGCTGCTAGCTCACCATCGCCTGCACACCGG
 CGGCCAGGACCCATTGGCGCTCGCAGTCAAGGAGCAGGTAATCCTCGTCGACGGACTCGGTAACCACGGCCAGC
 TCCGCTGCCAGGTCGGGGGTTGACACCGGGCATCGGATGGACGACGACGGCTGCTGACGGCGCTGTCG
 GACTCTGAGCTCGG (SEQ ID NO. 706)

:::::::::::::X0010T7.seq:::::::::::::

GGATGTGCTGTGAGCGCCGACCACCAAGCGCCGACGCTAAGGATGGAACGACGGCATCTCTGACGCGTAACCGCG
 TTGATCGCAGACTGAGGAGACGGTATGGGGAGGGTTCTGGAGGCCATCTGGATGTTGATGTCGATCTT
 GAGCCGGTCAACTCGTCGGCCGGACGGTACGCCGACGGCGAACGCCGCTACCCGTGACCTTCTGAGGAAAC
 GCTGCGTGGCTCACGAGATGATGGTGGTACCCCGCAGCTGGATACCGAATTGTCATCTGAGCAGGCCAGGGGG
 AAGCTGGCGTGTGACACGCCCTGTCGCGGGCAGGAAGCCGCGCAGGTGGTGCAGGCTTGCCTACGCAAACCGA
 CTGGTTGTTCCCC (SEQ ID NO. 707)

Clone X0012

:::::::::::::X0012SP6.seq:::::::::::::
 ATCACGACAACAGCGACGGTGTGTCGGATCAGGGCCCCCGTTGCCGGCAATGTTGAGGCCTTCTGCGTCTGGTT
 GAGGCCGGCTGGGAC-
 CCGAGGTGGCTCGCGGCCACATGGCAGCACACCACCGTGGTATGCATCTAGACGTGCAGGACCGTGGCGCTGGC
 CTGCA (SEQ ID NO. 708)

:::::::::::::X0012T7.seq:::::::::::::

GCGGCTACGTCCATCGAGACACTGGCGCAGGTATCGCACCCGTTATCGGCTGCGAGCAAATCGGGTATGCGTT
 TTGAGCATGAGTCGGCGACCGTGTGTCATGGTGCACACCCACGACGGAAAGACGCGAGATGCCGTCAAGCATGTC
 CGCGGATTATCAGGACTGACCTCCTGGCTGACCGGATGTTGGTCGCGATGCCCTG: (SEQ ID NO. 709)

Clone X00013

:::::::::::::X0013T7.seq:::::::::::::
 TACAAGCGGCACCTCGCCGGTGAACCTGACCGTTGCGACGCTGCGACCGCCGCCGGCGCTGCTCGCGCGCCGGC
 GGGCCCCCGAGGCCCTGAGAGGGGAACCAACCATGCAAGGTAAACCGCGAGGCCGTACCGCCGAGGTC
 CGAACCCCGGATGCTGCTGGTCCATTTCCTCGTGCAGCTGCCGTACCGGAAACTCACTGGGCTGTGATACCA
 GCAACTGCCGGACATGCCGTGGAGGTGACCGCGTGCACCGGCTGCCGGTAAATCCTGCACGATGCTGCCGTGATGCCCTCC
 GGGC (SEQ ID NO. 710)

Clone X0014

:::::::::::::X0014T7.seq:::::::::::::
 AGCGGCTGGTACGACTCCCTGTTGTGATGGACCACTTCTACCAACTGCCATGTTGGGACGCCG-CC-
 TCCGATGCTGGAAGCCTACACTGCCCTGGTGCCTGGCC-C-GCGACCGAGCGCTGCAACTGGGCGC-
 TTGGTGACC-GCAATACCTACCGCACCCC-ACCCCTGCTGG-CAAAC-
 ATCATCACACGCTGACTGGTTAGCGCCGGTGA-CGATCCTCGGCATTGGAACCGGTTGGTT- (SEQ ID NO. 711)

Clone X0015

:::::::::::::X0015SP6.seq:::::::::::::
 ACGCGCGCCGATCATATCTGCTATGGATGTACAATTGAGCTTCTGCTGTTACCACTGACGGCTGCTGATCCGACGCCG
 CTATGCTGACGTGTGAGATGCCGATCGGCCCTGGCTGACTCGGCCGGCTCTGGCTGATCCGACGCCG
 ATTCTGGTGGCGTTGCTGGATGGCGTTGCTATCCCGCCAGCTAGCTGCGCACCTGGGTTGACCCGATCGAATG
 GTCCAACCATCTGCGTGTGTTGCGGGCTGCCGGTGA-TCCCAACCTATGAGGGCCGGCAGGTTGGTAT
 (SEQ ID NO. 712)

:::::::X0015T7.seq:::::::
 CCGCGCTGCTGCTGACGTCGGTCGAACTGCGACACGTCTGCAATACCGGCCGAACGCTGGTTATCCACAGGCT
 GGCACCGACGCCACGACACACCCGGCGTCGCCGACCGCCACCGACTGCATCGGTGACGCCATTGGATCGCCGG
 TGCCCGGGCGCTGGAACCTGGCTGGGCTGGGCTCGATGACATCGAATACGTCGACCTGTATTCTGCTTCCTCCG
 CTGTCCAAGTCGCCGAATCGAATCGGCTGGACACCAGACGATCCTGCCGCCGCTGACCGTCACCGGGGCGCTG
 ACCTTCGCCGGCGGCGTGGAGCAATTACGTACGCACCTCCAT

(SEQ ID. NO. 713)

Clone X0016

:::::::X0016SP6.seq:::::::
 CAGGCCTGCAATGACCTGCACTGCGCCGGA-A-
 TCCCTAACCCACTAAACCGGGCGCTCACAAAGCCGTGCAAGCTCGGTGACGTCAGGTGCGCGACCAGGAA-
 TAAATGAGCAGACCCGTGCCGTCAACGATGGTGGCGATCATGGCCCGAACGATGGCGGGTC-
 ATGCGCAACTTCTTCAGCAGCGGCGGAAGGACGCGA-CCACCGAC-ACCACACCGAT

(SEQ ID NO. 714)

:::::::X0016T7.seq:::::::

CGCAA-
 CACTTCGTCAACTTCCAGGGCTGCCCGACCAAGTATTGACGAGTATTCCGTGGGGCGCCGCCGGCGCG
 GGCAGGTGGTCACTCTGGCGCGGGGCTGGACTCGCGCGTACCGGCTGCGCTGGCCGACGGGACCACGGTTTT
 GAGCTGGACCGCCCGCAGGTCTTGATTCAAGCGGAGGTGCTCGCCAGCCACGGTGGCCAACCGCGCGCCCTGCG
 CGCGAGATCGCGTCGACCTGCGTGACGATTGCCACAAGCTTGCAGGACAGTGGTTGATGCGGCTGACCGT
 CGGCATGGATTGCCGAAGGGCT

(SEQ ID NO. 715)

Clone X0017

:::::::X0017SP6.seq:::::::
 TTGGGC-TTGGCC-CAATA-GGCCCAATCAAAGCCGAGCAGGTGGAACCTA-CGCATTGCCTC-TCGT-
 TGTGCAACCGAGCCATCGCACGCGCGGGAAATTCCCGGAT-TC-
 CCGTATTCTCGGCGGCCGGGCTAACCCATCCCA-GCCGAACTGGTGGCTC-
 TGCGTGGGTCCCGTGTGGCGATCGGGCGTACCGGGGGTGTCTGGGTGCGG-TGACCATGGC-AACTGCC-
 ATGGGCCGACCCCTGGTGAGATAAACCTG

(SEQ ID NO. 716)

:::::::X0017T7.seq:::::::

TGGTGGAGGTCCCCACCAA-ACCCGGCCGTAACCTGCTCACGGAAATGCGG-
 CAGGCCGCGCGTAGCACGTGATCCGCCATAAAGGTGACCTTAAGCACGGCTCCAATTCTGAACGACATCTT
 GTGGAAGGTGCCGTCGCGCAAGATCCGGCGTTGCTCACACACCGTGCACGGCGCGAATTGTCAGCGCGGTCT
 TGATGATGTTGCTGCGCCGTCCTGGTGGCGACGCTGTCGGTA-
 TTGGCGACCGCCGGGCCCCCTTGCAGAAATCTCGGCGACGACCTCATCGGCCATGCCGAACCGGGCGCCG

(SEQ ID NO. 717)

Clone X0018

:::::::X0018SP6.seq:::::::
 GCCGGCCAAACTGGCGGGGGTGTGTC-TCAAGGTGGTTCCGCCACCAA-ACC-
 CACTCAAGGATCGCAAGGAAAGC-
 TCAAGGATGCGGTGCGGCCGCAAGGCCGCGTCAAGGAGGGCATCGTCCCTGGGGGA-
 CCTCCCTCATCCACCAGGCCGCAAGGCCGCTGACCGAATGC-TGCCTC-GACCGGTGACAA-
 GTCCTCGGTGTCACGTGT-CTCCGAAGCCCTGCCGTCCTGTTCTGGATC-CC-CCAAC-
 CTGGCTTGGACGGCTC-GTGGTGGTCAACAAGGTGAGCAGCTACCCGCCGGCATGGCTGAACGTGA

(SEQ ID NO. 718)

Clone X0018

:::::::X0018T7.seq:::::::
 CGAACCT-AATTGTCCTGTAATGCCAGCTACCAA-
 GCATGGCTGGTGGCGGGCGGTGAAGCCGGCTGCGGCCACCGTCAAATC-ATGTGGAT-
 GCCGGAAATGGGGATGTCGG-ACGGCGAATCCGTA-
 TTGCGTTGTCCTGAGGCCAGGTGGATGGGGGGAGGATC-TGGTGTCCGGGATGAT-
 ATGGGGCGATGCCGCCGGTTGAAGTCCACTGGATCGGAATTGTCGAT-CCGACGTTCAAGGCCGAAC

(SEQ ID NO. 719)

Clone X0019

:::::::::::X0019SP6.seq:::::::::::
 CTAACGGAATGAAAGCCCTGGTGGCCGT-
 TCGCGGTGGCCGTCGCACTGCTCGGTGTATCTCCGCCAAGCTGATCCGAGGCGGATCCGGCAGGTGA
 GGCAACTATGGTGGCCCCCAAGTTCCCCACGTCTGTCGATCACACCGAATGGCGCA-
 TGGGAATTCTGCCAGGCTCCGGGTCTACCGTCCCAAGTTGGCGTACA-
 CCTCCCGCCGCCCTCGGGATGGCGCTGCCGACCGGGCTGGCC-
 AGGTTCTCGCGCTGTCACCGGAAGCCGACACTGCCGGC (SEQ ID NO. 720)

:::::::::::X0019T7.seq:::::::::::
 CCGCGGGACAC-CCTC-
 ATGCTGCCGCATGGACCGGTCGAACGCAAGCAGCTGATCGAGCTACAACGCCGCGGAAACGCTTCCGCCGCGG
 CGTGACCGCATCCCGTTGACCGGGCGATCGCGGTGATCGTCGATGACGGCATGCCACCGGAGCGACGCCAAGGC
 GCGTGCCAGGTCGCCGGCGCACGGTGCAGGACAAGGTGGTGCCTGGCGTCCGATCGGCCA-
 ACGACATCGTGGCGAAGATTGCGGGTACGCCGATGATGTTGGTGTGTTGGCGACGCCGGTGTG (SEQ ID NO. 721)

Clone X0020

:::::::::::X0020T7.seq:::::::::::
 CTCTGGGACCGGCCACGGTGC-
 CCGCGTTCCCGGACGTGCTGCCGAGGTGTCGGCGCGCGTGCATGGTGTTCGGGATCGGCCGCTGGCCAGAG
 CCCACCGGTGAATCTGGCGCTGGCGACCACCGTGCCTGAGGCTTGCATCGTCAGCGCTGGCGTGGCCAGGA
 CGAGATCCGACGGATTGGGCAGATGCGTGCACCATCGGGTATTGACGGCGTGCACCGCGGGCACGCCGAAC
 TGATCGCGCACCGGTCAAAGCGGC (SEQ ID NO. 722)

Clone X0021

:::::::::::X0021SP6.seq:::::::::::
 AATACTCAAGCTTCTGTCAGTTGCAATTGCCAACGACCAACAA-AGCATCGGGACATACGGA-
 TCAACTACCCGGCCAACGGTGAATTCTTGGCCGCGCTGACGGCGCAACGACGCCAGCGACCAC-
 TTCAAGCAAATGGCCA-CGGTGCCGGCCACGAGGTTGGTGCCTGGCGCTACTCCACGGGTGCGGCCGTGATC-
 ACATC-TCACCGCCGACCAACTGCCCGCTCGGTTCACGCGACGGTGCCTGCCGAGCGGAC-
 ATCACATCGCCGCGATGCCCTGTTGGAAATCCCTC-GGCCGCGTGGCGGCTGATTAAAC (SEQ ID NO. 723)

:::::::::::X0021T7.seq:::::::::::
 TGGCGCGGATTGGCTGGCTGCCAATATTCAAATCGGGCCTTCTTTGCGCGACAATAAGGTACAGTAAACC
 CTCGTTTGTGAGATGCGGGCGGGCGGGCGAA-
 TCGACCTCGAGTGAATGGATCTCGAGTGAATGGACAGGGCATGCCCTACGAGTGCATCCCCATCCAACAGACGGT
 GCTTGTGCATCGGACCTGAAGGTCCCGCACGGAGGGTGTGGTTGCCGGCGGGGTACGGTGCCTGAGCTGA
 GTGTTGAACGAATTCTGATGCTCAACCTGTTGGTGTCAATCCAGTT (SEQ ID NO. 724)

Clone X0175

....X0175SP6....
 AA-CTTGCACGCTCGGGGGTC-AGCATCCAGCTGCTGCCAAGGAGGCCAGCTAC-C-
 TCGCTCGTATGCCAGCGGTGAGATCCGCCGGTC-
 ACGTCCGCTGCCGCGCACCGTCCGCGAAGTGGCAATGCCGAGCAGGCAAACATCAACTGGGCAAGGCCGGTCGG
 ATGCGGTGAAAGGGCAAGGCCGTCGGTCCGGCGTGGTGAT-AACCCGGTC-
 ACCACCGCACGGCGGTGGTGGGAAACCTCCGGCGGTACCCGGTTAGCCCGTGGGCAA (SEQ ID NO. 725)

....X0175T7....

A-TCGAAAGTGACCATCTACCTGAGTGCATACCGCCGACCCATGCCCTAGCTCGGATAGCTCGGCGAAAGAAACG
 CTTGCAGTGCCTGGCGAATAGGCAGCTACGTGAGCGCCCATCAACTCTCGCGGGAGTGCATGCCAGCTGGCG
 GCGCCGACGTCGACCGTGGGGATTCCGGTGCAGCGCCGCGCAACGGCCGATCGTCGACCCGACGGCAGATCGGC
 GCGATGTTCTGTAACGCTGCATAGGCACCTCCGCGCGTGGCAGGCCAGTGCAGCAGGCCGGTGCCTCG
 (SEQ ID NO. 726)

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CLAIMS

1. A method for isolating a polynucleotide of interest that is present in a genome of a first mycobacterium strain or that is expressed by said first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain that is different from the first mycobacterium strain or that is not expressed in the second mycobacterium strain, said method comprising:
 - a) contacting under hybridizing conditions the genomic DNA of the first mycobacterium strain with the DNA of at least one clone that belongs to a bacterial artificial chromosome (BAC) genomic DNA library of the second mycobacterium strain ; and
 - b) isolating the polynucleotide of interest that fails to form a hybrid with the DNA of the second mycobacterium strain.
2. The method according to claim 1, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium tuberculosis*.
3. The method according to claim 2, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium tuberculosis* strain H37Rv.
4. The method according to claim 3, wherein the BAC-based DNA library has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on November 19, 1997 under the accession number I-1945.
5. The method according to claim 1, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium bovis*.
6. The method according to claim 5, wherein the BAC-based DNA library has been constructed from the genomic DNA of *Mycobacterium bovis* BCG strain Pasteur.
7. The method according to claim 6, wherein the at least one BAC-based DNA library has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on XX XX, 1998 under the accession number I-XXXX.
8. A method of isolating a polynucleotide of interest that is present in a genome of a first mycobacterium strain or that is expressed by the first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain or that is not expressed by the second mycobacterium strain, said method comprising :

- a) providing at least one polynucleotide contained in a clone of a bacterial artificial chromosome (BAC) DNA library of the first mycobacterium strain;
- b) providing at least one genomic or cDNA polynucleotide from a second mycobacterium strain that is different from the first mycobacterium strain or at least one polynucleotide contained in a clone of a BAC DNA library prepared from the genome of the second mycobacterium strain;
- c) contacting under hybridizing conditions the polynucleotide of step a) with the polynucleotide of step b); and
- d) isolating the polynucleotide of step a) that has not formed a hybrid complex with the polynucleotide of step b).

9. The method of claim 8, wherein the polynucleotide contained in a clone of a BAC DNA library of the first or second mycobacterium strain is prepared by the following procedure :

- 1) digesting at least one recombinant BAC clone by an appropriate restriction endonuclease to yield a polynucleotide insert of interest; and
- 2) isolating the polynucleotide insert of interest.

10. A purified polynucleotide of interest that has been isolated according to the method of claim 8.

11. The purified polynucleotide of claim 10 which contains at least one Open Reading Frame (ORF).

12. The purified polynucleotide of claim 11, which is SEQ ID N0:1.

13. The purified polynucleotide of claim 11, wherein said polynucleotide is selected from the group consisting of :

- a) a polynucleotide comprising at least 8 consecutive nucleotides of SEQ ID N0:1 ;
- b) a polynucleotide having a sequence fully complementary to SEQ ID N°:1 ; and
- c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

14. The purified polynucleotide of claim 13, which is SEQ ID N0:2.

15. The purified polynucleotide of claim 13, which is SEQ ID N0:3.

16. The purified polynucleotide of claim 11, wherein the ORF encodes all or part of a polypeptide involved in the pathogenicity of a mycobacterium strain.

17. The purified polynucleotide of claim 11, wherein the ORF encodes all or part of a Polymorphism Glycine Rich Sequence (PGRS).

18. The purified polynucleotide of claim 17, which is SEQ ID N0:4.
19. The purified polynucleotide of claim 17, which is selected from the group consisting of :
 - 5 a) a polynucleotide comprising at least 8 consecutive nucleotides the of SEQ ID N0:5 ;
 - b) a polynucleotide having a sequence that is fully complementary to SEQ ID N0:5 ;
 - c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).
- 10 20. A pair of the purified polynucleotides as claimed in claim 10.
21. A *Mycobacterium tuberculosis* strain Rv37 genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes under accession number I-1945, wherein said genomic DNA library comprises recombinant bacterial artificial chromosome vectors.
- 15 22. A recombinant bacterial artificial chromosome (BAC) vector, which belongs to the genomic DNA library of claim 21.
23. The recombinant BAC vector of claim 22, which is selected from the group consisting of :
Rv101; Rv102; Rv103; Rv104; Rv105; Rv106; Rv107; Rv108; Rv109; Rv10;
20 Rv110; Rv111; Rv112; Rv113; Rv114; Rv115; Rv116; Rv117; Rv118; Rv119;
Rv11; Rv120; Rv121; Rv122; Rv123; Rv124; Rv126; Rv127; Rv128; Rv129;
Rv130; Rv132; Rv134; Rv135; Rv136; Rv137; Rv138; Rv139; Rv13; Rv140;
Rv141; Rv142; Rv143; Rv144; Rv145; Rv146; Rv147; Rv148; Rv149; Rv14;
25 Rv150; Rv151; Rv152; Rv153; Rv154; Rv155; Rv156; Rv157; Rv159; Rv15;
Rv160; Rv161; Rv162; Rv163; Rv164; Rv165; Rv166; Rv167; Rv169; Rv16;
Rv170; Rv171; Rv172; Rv173; Rv174; Rv175; Rv176; Rv177; Rv178; Rv179;
Rv17; Rv180; Rv181; Rv182; Rv183; Rv184; Rv185; Rv186; Rv187; Rv188;
Rv18; Rv190; Rv191; Rv192; Rv193; Rv194; Rv195; Rv196; Rv19; Rv1; Rv201;
Rv204; Rv205; Rv207; Rv209; Rv20; Rv214; Rv215; Rv217; Rv218; Rv219;
30 Rv21; Rv220; Rv221; Rv222; Rv223; Rv224; Rv225; Rv226; Rv227; Rv228;
Rv229; Rv22; Rv230; Rv231; Rv232; Rv233; Rv234; Rv235; Rv237; Rv240;
Rv241; Rv243; Rv244; Rv245; Rv246; Rv247; Rv249; Rv24; Rv251; Rv252;
Rv253; Rv254; Rv255; Rv257; Rv258; Rv259; Rv25; Rv260; Rv261; Rv262;
Rv263; Rv264; Rv265; Rv266; Rv267; Rv268; Rv269; Rv26; Rv270; Rv271;
35 Rv272; Rv273; Rv274; Rv275; Rv276; Rv277; Rv278; Rv279; Rv27; Rv280;

Rv281; Rv282; Rv283; Rv284; Rv285; Rv286; Rv287; Rv288; Rv289; Rv28;
Rv290; Rv291; Rv292; Rv293; Rv294; Rv295; Rv296; Rv29; Rv2; Rv301;
Rv302; Rv303; Rv304; Rv306; Rv307; Rv308; Rv309; Rv30; Rv310; Rv311;
Rv312; Rv313; Rv314; Rv315; Rv316; Rv317; Rv318; Rv319; Rv31; Rv32;
5 Rv322; Rv327; Rv328; Rv329; Rv32; Rv330; Rv331; Rv333; Rv334; Rv335;
Rv336; Rv337; Rv338; Rv339; Rv33; Rv340; Rv341; Rv343; Rv344; Rv346;
Rv347; Rv348; Rv349; Rv34; Rv350; Rv351; Rv352; Rv353; Rv354; Rv355;
Rv356; Rv357; Rv358; Rv359; Rv35; Rv360; Rv361; Rv363; Rv364; Rv365;
Rv366; Rv367; Rv368; Rv369; Rv36; Rv370; Rv371; Rv373; Rv374; Rv375;
10 Rv376; Rv377; Rv378; Rv379; Rv37; Rv381; Rv382; Rv383; Rv384; Rv385;
Rv386; Rv387; Rv388; Rv389; Rv38; Rv390; Rv391; Rv392; Rv393; Rv396;
Rv39; Rv3; Rv40; Rv412; Rv413; Rv414; Rv415; Rv416; Rv417; Rv418; Rv419;
Rv41; Rv42; Rv43; Rv44; Rv45; Rv46; Rv47; Rv48; Rv49; Rv4; Rv50; Rv51;
Rv52; Rv53; Rv54; Rv55; Rv56; Rv57; Rv58; Rv59; Rv5; Rv60; Rv61; Rv62;
15 Rv63; Rv64; Rv65; Rv66; Rv67; Rv68; Rv69; Rv6; Rv70; Rv71; Rv72; Rv73;
Rv74; Rv75; Rv76; Rv77; Rv78; Rv79; Rv7; Rv80; Rv81; Rv82; Rv83; Rv84;
Rv85; Rv86; Rv87; Rv88; Rv89; Rv8; Rv90; Rv91; Rv92; Rv94; Rv95; Rv96
and Rv9.

24. The recombinant BAC vector of claim 22, which is selected from the
20 group consisting of :

Rv234; Rv351; Rv166; Rv35; Rv415; Rv404; Rv209; Rv272; Rv30; Rv228;
Rv233; Rb38; Rv280; Rv177; Rv48; Rv374; Rv151; Rv238; Rv156; Rv92; Rv3;
Rv403; Rv322; Rv243; Rv330; Rv285; Rv233; Rv219; Rv416; Rv67; Rv222;
Rv149; Rv279; Rv87; Rv273; Rv266; Rv25; Rv136; Rv414; Rv13; Rv289; Rv60;
25 Rv104; Rv5; Rv165; Rv215; Rv329; Rv240; Rv19; Rv74; Rv411; Rv167; Rv56;
Rv80; Rv164; Rv59; Rv313; Rv265; Rv308; Rv220; Rv258; Rv339; Rv121;
Rv419; Rv418; Rv45; Rv217; Rv134; Rv17; Rv103; Rv21; Rv22; Rv2; Rv270;
Rv267; Rv174; Rv257; Rv44; Rv71; Rv7; Rv27; Rv191; Rv230; Rv128; Rv407;
Rv106; Rv39; Rv255; Rv74; Rv355; Rv268; Rv58; Rv173; Rv264; Rv417;
30 Rv401; Rv144; Rv302; Rv81; Rv163; Rv281; Rv221; Rv420; Rv175; Rv86;
Rv412; Rv73; Rv269; Rv214; Rv287; Rv42 and Rv143.

25. A *Mycobacterium bovis* BCG strain Pasteur genomic DNA library,
wherein said genomic DNA library comprises recombinant bacterial artificial
chromosome vectors.

26. A recombinant bacterial artificial chromosome (BAC) vector, which belongs to the genomic DNA library of claim 25.

27. A recombinant BAC vector according to claim 26, which is selected from the group consisting of :

5 X0001; X0002; X0003; X0004; X0006; X0007; X0008; X0009; X0010; X0012; X0013; X0014; X0015; X0016; X0017; X0018; X0019; X0020; X0021 and X0175.

28. A method for detecting a mycobacterial nucleic acid in a biological sample comprising the steps of :

10 a) contacting the recombinant BAC vector according to claim 22 or 26, or a purified polynucleotide according to claim 10 with the mycobacterial nucleic acid in the biological sample ; and
15 b) detecting a hybrid nucleic acid molecule formed between said recombinant BAC vector or said purified polynucleotide and the mycobacterial nucleic acid in the biological sample.

29. The method of claim 28, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization reaction.

30. A method for detecting mycobacterial nucleic acid in a biological sample comprising the steps of :

a) contacting a first polynucleotide according to claim 10 that has been immobilized onto a substrate with the mycobacterial nucleic acid in the biological sample ; and

25 b) contacting a hybrid nucleic acid molecule formed between said first polynucleotide and the mycobacterial nucleic acid in the biological sample with a second, labeled polynucleotide according to claim 10, wherein said second polynucleotide and said first polynucleotide have non-overlapping sequences.

31. The method of claim 30, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization reaction.

32. The method of claim 30 or 31, further comprising before step b), removing the mycobacterial nucleic acid that is not hybridized with the immobilized first polynucleotide.

33. A method for detecting mycobacterial nucleic acid in a biological sample comprising the steps of :

- a) contacting the mycobacterial nucleic acid in the biological sample with a pair of purified polynucleotides according to claim 20 ;
- b) amplifying said mycobacterial nucleic acid ; and
- c) detecting the amplified mycobacterial nucleic acid.

5 34. The method of claim 33, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization reaction.

35. A kit for detecting a mycobacterium in a biological sample comprising :

10 a) a recombinant BAC vector according to claim 22 or 26, or a purified polynucleotide according to claim 10 ; and

b) reagents necessary to perform a nucleic acid hybridization reaction.

36. A kit for detecting a mycobacterium in a biological sample comprising :

15 a) a recombinant BAC vector according to claim 22 or 26, or a first polynucleotide according to claim 10 that is immobilized onto a substrate ;

b) reagents necessary to perform a nucleic acid hybridization reaction ; and

c) a second polynucleotide according to claim 10, wherein said second polynucleotide is radioactively or non-radioactively labeled, and wherein said second polynucleotide and said first polynucleotide have non-overlapping sequences.

20 37. A kit for detecting a mycobacterium in a biological sample comprising :

a) a pair of purified polynucleotides according to claim 20 ; and

25 b) reagents necessary to perform a nucleic acid amplification reaction.

38. A method for detecting the presence of a genomic DNA, a cDNA or a mRNA of a mycobacterium in a biological sample, comprising the steps of :

30 a) contacting the biological sample with a plurality of BAC vectors according to claim 22 or 26, or purified polynucleotides according to claim 10 that are immobilized on a substrate ; and

b) detecting the hybrid complexes formed.

39. A kit for detecting a genomic DNA, a cDNA or a mRNA of a mycobacterium in a biological sample, comprising :

35 a) a substrate on which a plurality of BAC vectors according to claim 22 or 26, or purified polynucleotides according to claim 10 have been immobilized.

40. A method for detecting a polynucleotide of mycobacterial origin in a biological sample, said method comprising :

a) aligning at least one polynucleotide contained in a recombinant BAC vector according to claim 22 or 26 on the surface of a substrate ;

5 b) contacting the polynucleotide in the biological sample with the substrate on which the polynucleotide of step a) has been aligned ; and

c) detecting a hybrid nucleic acid molecule formed between the polynucleotide in the biological sample and the aligned polynucleotide of step a).

41. A kit for detecting a polynucleotide of mycobacterial origin in a biological sample, comprising :

a) a substrate on which at least one polynucleotide contained in a recombinant BAC vector according to claim 22 or 26 has been aligned.

42. The method of claim 9, wherein the procedure by which the polynucleotide contained in a clone of a BAC DNA library is prepared, further comprises amplifying the polynucleotide insert.

43. The method of claim 9, wherein the procedure by which the polynucleotide contained in a clone of a BAC DNA library is prepared, further comprises digesting the polynucleotide insert with at least one restriction endonuclease.

20 44. The method of claim 42, further comprising digesting the amplified polynucleotide insert with at least one restriction endonuclease.

45. The Polynucleotide of claim 16, wherein the mycobacterium strain is *Mycobacterium tuberculosis*.

46. The method of claim 33, wherein the amplified mycobacterial DNA is 25 detected by gel electrophoresis or with a labeled polynucleotide according to claim 10.

47. The kit of claim 37, further comprising a polynucleotide according to claim 10.

48. The kit of claim 39, further comprising reagents necessary to perform a 30 hybridization reaction.

49. A method for physically mapping a polynucleotide of mycobacterial origin in a biological sample, said method comprising:

a) aligning at least one polynucleotide contained in a recombinant BAC vector according to claim 22 or 26 on the surface of a substrate;

- b) contacting the polynucleotide in the biological sample with the substrate on which the polynucleotide of step a) has been aligned under hybridizing conditions; and
- c) detecting the location of the hybridized polynucleotide from the biological sample.

5 50. The kit of claim 41, further comprising reagents necessary for labeling DNA and reagents necessary for performing a hybridization reaction.